

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 17.8241 Seconds  
(without alignments)  
770.608 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193  
Perfect score: 943  
Sequence: 1 CNAPRWVSLMVLVAIGTAVT.....HVHISKSKVGLQLPHKKI 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	243	1	US-07-915-720D-16
2	943	100.0	243	3	US-09-025-543-16
3	943	100.0	262	4	US-09-949-016-9146
4	943	100.0	300	1	US-08-218-026-2
5	943	100.0	300	2	US-08-653-632-2
6	943	100.0	368	1	US-07-915-720D-15
7	943	100.0	368	3	US-09-025-543-15
8	943	100.0	483	4	US-09-578-063-38
9	943	100.0	487	1	US-08-030-644-2
10	943	100.0	487	1	US-08-013-801-2
11	943	100.0	487	1	US-08-072-063-2
12	943	100.0	487	1	US-08-212-132-2
13	943	100.0	487	1	US-08-414-924-2
14	943	100.0	487	1	US-08-311-611A-69
15	943	100.0	487	1	US-08-311-611A-146
16	943	100.0	487	1	US-08-173-968-2
17	943	100.0	487	1	US-08-232-527-2
18	943	100.0	487	1	US-08-372-783-69
19	943	100.0	487	1	US-08-372-783-146
20	943	100.0	487	1	US-08-372-105-69
21	943	100.0	487	1	US-08-372-105-146
22	943	100.0	487	1	US-08-415-158-2
23	943	100.0	487	1	US-08-064-693-2
24	943	100.0	487	1	US-08-291-112-2
25	943	100.0	487	1	US-08-306-473A-69
26	943	100.0	487	1	US-08-306-473A-146
27	943	100.0	487	1	US-08-430-417-2

28	943	100.0	487	1	US-08-557-287-2	Sequence 2, Appli
29	943	100.0	487	1	US-08-470-366-2	Sequence 2, Appli
30	943	100.0	487	1	US-08-261-660A-12	Sequence 12, Appl
31	943	100.0	487	1	US-08-209-762-69	Sequence 69, Appl
32	943	100.0	487	1	US-08-644-290-2	Sequence 2, Appli
33	943	100.0	487	1	US-08-378-228-2	Sequence 2, Appli
34	943	100.0	487	1	US-08-927-438-2	Sequence 2, Appli
35	943	100.0	487	1	US-08-473-344-69	Sequence 69, Appl
36	943	100.0	487	1	US-08-274-303-2	Sequence 2, Appli
37	943	100.0	487	1	US-07-915-720D-13	Sequence 13, Appl
38	943	100.0	487	1	US-08-218-026-4	Sequence 4, Appli
39	943	100.0	487	1	US-08-435-855-2	Sequence 2, Appli
40	943	100.0	487	2	US-08-466-822-2	Sequence 2, Appli
41	943	100.0	487	2	US-08-653-632-4	Sequence 4, Appli
42	943	100.0	487	2	US-08-466-624-2	Sequence 2, Appli
43	943	100.0	487	2	US-08-621-803-265	Sequence 265, App
44	943	100.0	487	2	US-08-466-826-2	Sequence 2, Appli
45	943	100.0	487	2	US-08-704-504-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-07-915-720D-16  
; Sequence 16, Application US/07915720D  
; Patent No. 5770694  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W.  
; APPLICANT: Marra, Marian N.  
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 2200 Sand Hill Road, Suite 100  
; CITY: Menlo Park  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/915,720D  
; FILING DATE: 22-JUL-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L.  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/DOCKET NUMBER: 06514/030001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/322-5070  
; TELEFAX: 415/854-0875  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-915-720D-16

Query Match 100.0%; Score 943; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 4.7e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAAVNPVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60  
DB 10 CNAPRWVSLMVLVAIGTAVTAAVNPVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69

QY 61 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 189  
QY 181 HKKI 184  
Db 190 HKKI 193  
RESULT 2  
US-09-025-543-16  
; Sequence 16, Application US/09025543  
; Patent No. 6093801  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W.  
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bozicevic & Reed, LLP  
; STREET: 285 Hamilton, Suite 200  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,543  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Francis, Carol L.  
; REGISTRATION NUMBER: 36,513  
; REFERENCE/DOCKET NUMBER: 06514/030005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/327-3400  
; TELEFAX: 650/327-3231  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 243 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-025-543-16  
Query Match 100.0%; Score 943; DB 3; Length 243;  
Best Local Similarity 100.0%; Pred. No. 4.7e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69  
QY 61 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 189  
QY 181 HKKI 184  
Db 190 HKKI 193

Db 190 HKKI 193  
RESULT 3  
US-09-949-016-9146  
; Sequence 9146, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9146  
; LENGTH: 262  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-9146  
Query Match 100.0%; Score 943; DB 4; Length 262;  
Best Local Similarity 100.0%; Pred. No. 5.1e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 33 CNAPRWVSLMVLVAIGTAVTAANNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 92  
QY 61 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 120  
Db 93 DSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFL 152  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 180  
Db 153 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHHSKSKVGLIQLF 212  
QY 181 HKKI 184  
Db 213 HKKI 216  
RESULT 4  
US-08-218-026-2  
; Sequence 2, Application US/08218026  
; Patent No. 5786324  
; GENERAL INFORMATION:  
; APPLICANT: Gray, Beulah  
; APPLICANT: Hasegan, Judith R.  
; APPLICANT: Mayo, Kevin  
; TITLE OF INVENTION: Synthetic Peptides with Bactericidal  
; Activity and Endotoxin Neutralizing Activity for Gram  
; Negative Bacteria and Methods for Their Use  
; NUMBER OF SEQUENCES: 60  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merchant & Gould  
; STREET: 3100 No. 5786324west Center  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,026
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.286US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-218-026-2

Query Match 100.0%; Score 943; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60
Db |||||
QY 10 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69
Db |||||
QY 61 DSFKIKHLKGHYSFYSDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 120
Db |||||
QY 70 DSFKIKHLKGHYSFYSDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 129
Db |||||
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVGLIQLF 180
Db |||||
QY 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVGLIQLF 189
QY 181 HKKI 184
Db |||||
QY 190 HKKI 193
Db |||||

RESULT 5
US-08-653-632-2
; Sequence 2, Application US/08653632
; Patent No. 5830860
; GENERAL INFORMATION:
; APPLICANT: GRAY, Beulah
; APPLICANT: HASEMAN, Judith R.
; APPLICANT: MAYO, Kevin
; TITLE OF INVENTION: PEPTIDES WITH BACTERICIDAL AND ENDOTOXIN NEUTRALIZING
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 5830860west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,632
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/218026
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Kettelberger, Denise M
; REGISTRATION NUMBER: 33,924
; REFERENCE/DOCKET NUMBER: 600.286US11
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5268
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-653-632-2

Query Match 100.0%; Score 943; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60
Db |||||
QY 10 CNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69
Db |||||
QY 61 DSFKIKHLKGHYSFYSDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 120
Db |||||
QY 70 DSFKIKHLKGHYSFYSDIREFQLPSSQISMVNVNGLKFSISNANIKISGKWKAKQKRF 129
Db |||||
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVGLIQLF 180
Db |||||
QY 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVGLIQLF 189
QY 181 HKKI 184
Db |||||
QY 190 HKKI 193
Db |||||

RESULT 6
US-07-915-720D-15
; Sequence 15, Application US/07915720D
; Patent No. 5770694
; GENERAL INFORMATION:
; APPLICANT: Scott, Randal W.
; APPLICANT: Marra, Marian N.
; TITLE OF INVENTION: GENETICALLY ENGINEERED BPI VARIANT
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Fish & Richardson, P.C.
; STREET: 2200 Sand Hill Road, Suite 100
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,720D
; FILING DATE: 22-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513
; REFERENCE/DOCKET NUMBER: 06514/030001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/322-5070
; TELEFAX: 415/854-0875
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 368 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-915-720D-15

Query Match      100.0%; Score 943; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 7.3e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 69

Qy 61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 70 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180
   |||||
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189

Qy 181 HKKI 184
   |||||
Db 190 HKKI 193

RESULT 8
US-09-578-063-38
; Sequence 38, Application US/09578063
; Patent No. 6764677
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A
; APPLICANT: Barnes, Thomas M
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; FILE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 210147.0023/6U1
; CURRENT APPLICATION NUMBER: US/09/578,063
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-578-063-38

Query Match      100.0%; Score 943; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 9.8e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 60
   |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS 65

Qy 61 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120
   |||||
Db 66 DSFKIKHLGKGHYSFYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 125

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180
   |||||
Db 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 185

Qy 181 HKKI 184
   |||||
Db 186 HKKI 189

RESULT 9
US-08-030-644-2
; Sequence 2, Application US/08030644
; Patent No. 5348942
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G. II
; APPLICANT: Gazzano-Santoro, Helene
; APPLICANT: Parent, James Brian
; TITLE OF INVENTION: Therapeutic uses of
; Bactericidal/Permeability-Increasing Protein Products
```



```
; FILING DATE: 19930519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-072-063-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
Qy 61 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 12
US-08-212-132-2
; Sequence 2, Application US/08212132
; Patent No. 5447913
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Ammons, William Steve
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Dimer Products
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,132
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/31735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-072-063-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
Qy 61 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 13
US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896
; GENERAL INFORMATION:
; APPLICANT: Hansbrough, John F.
; TITLE OF INVENTION: Method of Treating Conditions
; TITLE OF INVENTION: Associated With Burn Injuries
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,924
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32297
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-414-924-2

Query Match 100.0%; Score 943; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 9.9e-70;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69
Qy 61 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120
Db 70 DSPKIKHLGKGHSFYSDMIREFQLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193
```

	Matches	184;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	CNAPRWYSLMLVLAIGTAVTA	AAVNPVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS	60						
Db	10	CNAPRWYSLMLVLAIGTAVTA	AAVNPVVVRISQKGLDYASQOGTAALQKELKRIKIPDYS	69						
Qy	61	DSFKIKHLKGCHYSFYSMDIRE	FOLPSQISMPNVNGLKFSISVANIKISGKWKAAQKRF	120						
Db	70	DSFKIKHLKGCHYSFYSMDIRE	FOLPSQISMPNVNGLKFSISVANIKISGKWKAAQKRF	129						
Qy	121	KMSGNFDLSLEGMSISADLKL	GSNPTSGKPTITCSSCSSHINSVHVHISKS	180						
Db	130	KMSGNFDLSLEGMSISADLKL	GSNPTSGKPTITCSSCSSHINSVHVHISKS	189						
Qy	181	HKKI	184							
Db	190	HKKI	193							

```

RESULT 14
US-08-311-611A-69
; Sequence 69, Application US/08311611A
; Patent No. 5523288
; GENERAL INFORMATION:
; APPLICANT: Cohen, Jonathan
; APPLICANT: Kung, Ada H.C.
; APPLICANT: Lambert, Jr., Lewis H.
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial
; TITLE OF INVENTION: Infection by Administration of
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,611A
; FILING DATE:
; PRIOR APPLICATION NUMBER: 08/273,401
; APPLICATION DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/125,651
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 32251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "FBPI"
US-08-311-611A-69

```

Query Match  
100.0%; Score 943; DB 1; Length 487;

		Best Local Similarity	100.0%;	Pred. No. 9.9e-70;	Mismatches	0;	Indels	0;	Gaps	0
		Matches	184;	Conservative	0;					
Qy	1	CNAPRWVSLMVLVAIGTAVTA	VAAVNPVVVRISQKGLDYASQQGTAALQKEIKRIKIPDYS	60						
Dd	10	CNAPRWVSLMVLVAIGTAVTA	VAAVNPVVVRISQKGLDYASQQGTAALQKEIKRIKIPDYS	69						
Qy	61	DSPFKI KHLKGHYSFYSDMR	EFPQLPSSQSISMVNVGLKFPSISNANI KISGKWKAQKRFL	120						
Dd	70	DSPFKI KHLKGHYSFYSDMR	EFPQLPSSQSISMVNVGLKFPSISNANI KISGKWKAQKRFL	129						
Qy	121	KMSGNFPLSTEGHMSIADLKL	GSNPTSGKPITICSSCSHHNSVHVHLSKSKVGWLIOLF	180						
Dd	130	KMSGNFPLSTEGHMSIADLKL	GSNPTSGKPITICSSCSHHNSVHVHLSKSKVGWLIOLF	189						
Qy	181	HKKI	184							
Dd	190	HKKI	193							

RESULT 15  
 US-08-311-611A-146  
 ; Sequence 146, Application US/08311611A  
 ; Patent No. 5523288  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cohen, Jonathan  
 ; APPLICANT: Kung, Ada H.C.  
 ; APPLICANT: Lambert, Jr., Lewis H.  
 ; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
 ; TITLE OF INVENTION: Infection by Administration of  
 ; TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
 ; TITLE OF INVENTION:  
 ; NUMBER OF SEQUENCES: 227  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60606-6402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/311,611A  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/273,401  
 ; FILING DATE: 11-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/125,651  
 ; FILING DATE: 22-SEP-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharp, Jeffrey S.  
 ; REGISTRATION NUMBER: 31,879  
 ; REFERENCE/DOCKET NUMBER: 32251  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ; INFORMATION FOR SEQ ID NO: 146:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 487 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-311-611A-146

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels

**Gaps**      **0;**

Qy	1	CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOGTAALQKELKIKIPDYS	60
Db	10	CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOGTAALQKELKIKIPDYS	69
Qy	61	DSFKIKHLGKGHSFYSDIREFOLPSSQISMVFNVLKFSISNANIKISGKWKAKRFL	120
Db	70	DSFKIKHLGKGHSFYSDIREFOLPSSQISMVFNVLKFSISNANIKISGKWKAKRFL	129
Qy	121	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF	180
Db	130	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGWLIQLF	189
Qy	181	HKKI 184	
Db	190	HKKI 193	

Search completed: October 21, 2005, 11:32:58  
Job time : 18.8241 secs



NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030.644  
FILING DATE: 19930312  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 31229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-644-2

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
  
Qy 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 189  
  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 10  
US-08-013-801-2  
Sequence 2, Application US/08013801  
Patent No. 5420019  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Horwitz, Arnold  
APPLICANT: Burke, David  
APPLICANT: Baltaian, Manik  
APPLICANT: Grinna, Lynn S  
TITLE OF INVENTION: Stable Bactericidal/Permeability-  
TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical  
TITLE OF INVENTION: Compositions Containing the Same  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza  
CITY: Chicago

STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/013.801  
FILING DATE: 02 FEB 1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyers, Thomas C.  
REGISTRATION NUMBER: P-36,989  
REFERENCE/DOCKET NUMBER: 27129/30911  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/346-5750  
TELEFAX: 312/346-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-013-801-2

Query Match 100.0%; Score 943; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 9.9e-70;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
  
Qy 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
Db 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHLSKSKVGLIQLF 189  
  
Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 11  
US-08-072-063-2  
Sequence 2, Application US/08072063  
Patent No. 5439807  
GENERAL INFORMATION:  
APPLICANT: Theofan, Georgia  
APPLICANT: Grinna, Lynn S  
APPLICANT: Horwitz, Arnold  
TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/072.063



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 47.1759 Seconds  
(without alignments)  
770.608 Million cell updates/sec

Title: US-10-629-516-2

Perfect score: 2507

Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQPHQNFLLFGADVYK 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507	100.0	487	1	US-08-030-644-2
2	2507	100.0	487	1	US-08-013-801-2
3	2507	100.0	487	1	US-08-072-063-2
4	2507	100.0	487	1	US-08-212-132-2
5	2507	100.0	487	1	US-08-414-924-2
6	2507	100.0	487	1	US-08-311-611A-69
7	2507	100.0	487	1	US-08-311-611A-146
8	2507	100.0	487	1	US-08-173-968-2
9	2507	100.0	487	1	US-08-232-527-2
10	2507	100.0	487	1	US-08-372-783-69
11	2507	100.0	487	1	US-08-372-783-146
12	2507	100.0	487	1	US-08-372-105-69
13	2507	100.0	487	1	US-08-372-105-146
14	2507	100.0	487	1	US-08-415-158-2
15	2507	100.0	487	1	US-08-064-693-2
16	2507	100.0	487	1	US-08-291-112-2
17	2507	100.0	487	1	US-08-306-473A-69
18	2507	100.0	487	1	US-08-306-473A-146
19	2507	100.0	487	1	US-08-430-417-2
20	2507	100.0	487	1	US-08-557-287-2
21	2507	100.0	487	1	US-08-470-366-2
22	2507	100.0	487	1	US-08-261-660A-12
23	2507	100.0	487	1	US-08-209-762-69
24	2507	100.0	487	1	US-08-644-290-2
25	2507	100.0	487	1	US-08-378-228-2
26	2507	100.0	487	1	US-08-927-438-2
27	2507	100.0	487	1	US-08-473-344-69

28	2507	100.0	487	1	US-08-274-303-2	Sequence 2, Appli
29	2507	100.0	487	1	US-07-915-720D-13	Sequence 13, Appli
30	2507	100.0	487	1	US-08-435-855-2	Sequence 2, Appli
31	2507	100.0	487	2	US-08-466-822-2	Sequence 2, Appli
32	2507	100.0	487	2	US-08-466-624-2	Sequence 2, Appli
33	2507	100.0	487	2	US-08-621-803-265	Sequence 265, App
34	2507	100.0	487	2	US-08-466-826-2	Sequence 2, Appli
35	2507	100.0	487	2	US-08-704-504-2	Sequence 2, Appli
36	2507	100.0	487	2	US-08-485-445A-69	Sequence 69, Appli
37	2507	100.0	487	2	US-08-485-445A-146	Sequence 146, App
38	2507	100.0	487	2	US-08-621-259A-252	Sequence 252, App
39	2507	100.0	487	2	US-08-586-133-2	Sequence 2, Appli
40	2507	100.0	487	2	US-09-063-465-2	Sequence 2, Appli
41	2507	100.0	487	2	US-08-862-785A-2	Sequence 2, Appli
42	2507	100.0	487	2	US-09-081-166-2	Sequence 2, Appli
43	2507	100.0	487	2	US-09-203-159-2	Sequence 2, Appli
44	2507	100.0	487	3	US-09-099-725-2	Sequence 2, Appli
45	2507	100.0	487	3	US-08-756-164-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-08-030-644-2  
; Sequence 2, Application US/08030644  
; Patent No. 5348942  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G. II  
; APPLICANT: Gazzano-Santoro, Helene  
; APPLICANT: Parent, James Brian  
; TITLE OF INVENTION: Therapeutic uses of  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/030,644  
; FILING DATE: 19930312  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shaip, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 31229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-030-644-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENARGPCNAPRWVSLMVLAIGTAVTAAPNGVVRISQKGLDYASQCGTAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLAIGTAVTAAPNGVVRISQKGLDYASQCGTAALQKEL 60

QY 61 KRIPDYSDSPFKIHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120  
DB 61 KRIPDYSDSPFKIHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120  
QY 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
DB 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
QY 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240  
DB 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240  
QY 241 VAPPATTAETLDVQMGKEFYSENHNHPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTAETLDVQMGKEFYSENHNHPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300  
QY 301 YQAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
DB 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
QY 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480  
DB 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

## RESULT 2

US-08-013-801-2  
; Sequence 2, Application US/08013801  
; Patent No. 5420019  
; GENERAL INFORMATION:  
; APPLICANT: Theofan, Georgia  
; APPLICANT: Horwitz, Arnold  
; APPLICANT: Burke, David  
; APPLICANT: Baltanian, Manik  
; APPLICANT: Grinna, Lynn S  
; TITLE OF INVENTION: Stable Bactericidal/Permeability-  
; TITLE OF INVENTION: Increasing Protein Products and Pharmaceutical  
; TITLE OF INVENTION: Compositions Containing the Same  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/013.801  
; FILING DATE: 02 FEB 1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyers, Thomas C.  
; REGISTRATION NUMBER: P-36,989  
; REFERENCE/DOCKET NUMBER: 27129/30911  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/346-5750  
; TELEFAX: 312/346-9740  
; TELEX: 25-3856

## ; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-013-801-2

Query Match 100.0%; Score 2507; DB 1; Length 487;

Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENMAAGPCNAPRWYSLMVLVAIGTAVTAAGVNVVVRISQKGLDYASOQGTAAQKEL 60  
DB 1 MRENMAAGPCNAPRWYSLMVLVAIGTAVTAAGVNVVVRISQKGLDYASOQGTAAQKEL 60  
QY 61 KRIPDYSDSPFKIHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120  
DB 61 KRIPDYSDSPFKIHLGKHGHSFYSDIRFQLPSSQISMVNVNGLKFSISNANIKISG 120  
QY 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
DB 121 KWAQKRFLLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
QY 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240  
DB 181 KVGWLIQLPHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240  
QY 241 VAPPATTAETLDVQMGKEFYSENHNHPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTAETLDVQMGKEFYSENHNHPPPPAPPVMEFPAADRMVYLGSLDYFFNTAGLV 300  
QY 301 YQAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLKMTLRDDMIKESKFRLLTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
DB 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
QY 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480  
DB 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLOKGFPLTPPARVOLYNNVVLQPHQNFLLF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

## RESULT 3

US-08-072-063-2  
; Sequence 2, Application US/08072063  
; Patent No. 5439807  
; GENERAL INFORMATION:  
; APPLICANT: Theofan, Georgia  
; APPLICANT: Grinna, Lynn S  
; APPLICANT: Horwitz, Arnold  
; TITLE OF INVENTION: BPI-immunoglobulin Fusion Proteins  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/072,063

```

; FILING DATE: 19930519
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-072-063-2

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIQKGLDYASQOQTAALQKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKIQKGFPLTPARVOLYNNVQLPHQNFLLF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKIQKGFPLTPARVOLYNNVQLPHQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

```

```

RESULT 4
US-08-212-132-2
; Sequence 2, Application US/08212132
; Patent No. 5447913
; GENERAL INFORMATION:
; APPLICANT: Little, Roger G.
; APPLICANT: Ammons, William Steve
; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability-
; TITLE OF INVENTION: Increasing Protein Dimer Products
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago

```

```

; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212.132
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/31735
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-212-132-2

```

```

Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIQKGLDYASQOQTAALQKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVWVRIQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSPYSMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKGNSPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKIQKGFPLTPARVOLYNNVQLPHQNFLLF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKIQKGFPLTPARVOLYNNVQLPHQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

```

```

RESULT 5
US-08-414-924-2
; Sequence 2, Application US/08414924
; Patent No. 5494896

```

GENERAL INFORMATION:  
APPLICANT: Hansbrough, John F.  
TITLE OF INVENTION: Method of Treating Conditions  
TITLE OF INVENTION: Method of Treating Conditions  
TITLE OF INVENTION: Associated With Burn Injuries  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/414,924  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 27129/32297  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-414-924-2

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANVPVGVVRSQKGLDYASQGGTAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANVPVGVVRSQKGLDYASQGGTAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKNNSOVCEKVTNSVSKLPYFQTLVMTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKNNSOVCEKVTNSVSKLPYFQTLVMTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGEFFYSNHNPPPPAPPVMEFPAAHDMVYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGEFFYSNHNPPPPAPPVMEFPAAHDMVYLGLSDYFFNTAGLV 300  
Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGTFLPEVAKKPNMKIQIHVSASTPPLHSVQ 360  
Db 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGTFLPEVAKKPNMKIQIHVSASTPPLHSVQ 360  
Qy 361 PTGLTFTFPAVDVQFAVLV PNSSLASLFLIGHMTTGSMEVSAESNRLV GELKLDRLLELK 420  
Db 361 PTGLTFTFPAVDVQFAVLV PNSSLASLFLIGHMTTGSMEVSAESNRLV GELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDQIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLPQHONFLF 480  
Db 421 HSNIGPPFVELLDQIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLPQHONFLF 480

Qy 481 GADVVK 487  
Db 481 GADVVK 487  
RESULT 6  
US-08-311-611A-69  
Sequence 69, Application US/08311611A  
Patent No. 5523288  
GENERAL INFORMATION:  
APPLICANT: Cohen, Jonathan  
APPLICANT: Kung, Ada H.C.  
APPLICANT: Lambert, Jr., Lewis H.  
TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
TITLE OF INVENTION: Infection by Administration of  
TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606-6402  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/311,611A  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,401  
FILING DATE: 11-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/125,651  
FILING DATE: 22-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Sharp, Jeffrey S.  
REGISTRATION/DOCKET NUMBER: 31,879  
REFERENCE/DOCKET NUMBER: 32251  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: "rBPI"  
US-08-311-611A-69

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANVPVGVVRSQKGLDYASQGGTAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAANVPVGVVRSQKGLDYASQGGTAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLKGHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180

Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTMKIDS VAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTMKIDS VAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGFYSNNHNPFPFPPVMEFFAAHDMVYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGFYSNNHNPFPFPPVMEFFAAHDMVYLGLSDYFFNTAGLV 300  
Qy 301 YQAGVLKMTLDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPLHSVQ 360  
Db 301 YQAGVLKMTLDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPLHSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
Qy 421 HSNIGPPFVELLQDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLQDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 7

US-08-311-611A-146  
; Sequence 146, Application US/08311611A  
; Patent No. 5523288  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Jonathan  
; APPLICANT: Kung, Ada H.C.  
; APPLICANT: Lambert, Jr., Lewis H.  
; TITLE OF INVENTION: Method for Treating Gram-Negative Bacterial  
; TITLE OF INVENTION: Infection by Administration of  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing  
; TITLE OF INVENTION:  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/311,611A  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/273,401  
; FILING DATE: 11-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/125,651  
; FILING DATE: 22-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Shaip, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 32251  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 146:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-311-611A-146  
Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0;  
Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQTAAQLKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQTAAQLKEL 60  
Qy 61 KRIKIPDYSDFKIKHLGKGHYSFYSDIRFQLPSSQISMVNPVGLKFSINAIKISG 120  
Db 61 KRIKIPDYSDFKIKHLGKGHYSFYSDIRFQLPSSQISMVNPVGLKFSINAIKISG 120  
Qy 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Db 121 KWKAQKRLKMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTMKIDS VAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVTMKIDS VAGINYL 240  
Qy 241 VAPPATTAETLDVQMKGFYSNNHNPFPFPPVMEFFAAHDMVYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGFYSNNHNPFPFPPVMEFFAAHDMVYLGLSDYFFNTAGLV 300  
Qy 301 YQAGVLKMTLDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPLHSVQ 360  
Db 301 YQAGVLKMTLDDMI PKESKRLTTKFGTFLPEVAKKFNPKIQIHVSASTPPLHSVQ 360  
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420  
Qy 421 HSNIGPPFVELLQDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLQDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487  
RESULT 8  
US-08-173-968-2  
; Sequence 2, Application US/08173968  
; Patent No. 5576292  
; GENERAL INFORMATION:  
; APPLICANT: Elsbach, Peter  
; APPLICANT: Weiss, Jerrold  
; TITLE OF INVENTION: Biologically Active  
; TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Fragments  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howard M. Frankfort  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173,968  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/754,204

```
; FILING DATE: 26-AUG-1991
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Frankfort, Howard M.
; REGISTRATION NUMBER: 32,613
; REFERENCE/DOCKET NUMBER: 5969/05982US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: blood
; CELL TYPE: promyelocytic leukemia cells
; US-08-173-968-2
```

```
Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRIPIDYDSFKIKHLGKGHSFYSDMDIREFQLPSSQISKVPNVNGLKFSISNANIKISG 120
DB 61 KRIPIDYDSFKIKHLGKGHSFYSDMDIREFQLPSSQISKVPNVNGLKFSISNANIKISG 120

QY 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGHLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
DB 181 KVGHLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSLDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSLDYFNTAGLV 300

QY 301 QEAGVLKMTLRDDMIKESKFRLLTKFQFTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 QEAGVLKMTLRDDMIKESKFRLLTKFQFTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELKL 420
DB 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELKL 420

QY 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVNVLQPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVNVLQPHQNFLLF 480

QY 481 GADVYK 487
DB 481 GADVYK 487
```

```
RESULT 9
US-08-232-527-2
; Sequence 2, Application US/08232527
; Patent No. 5578568
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
```

```
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,527
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-232-527-2
```

```
Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQGGTAALQKEL 60

QY 61 KRIPIDYDSFKIKHLGKGHSFYSDMDIREFQLPSSQISKVPNVNGLKFSISNANIKISG 120
DB 61 KRIPIDYDSFKIKHLGKGHSFYSDMDIREFQLPSSQISKVPNVNGLKFSISNANIKISG 120

QY 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
DB 121 KWAKQKFLKWSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

QY 181 KVGHLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
DB 181 KVGHLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSLDYFNTAGLV 300
DB 241 VAPPATTAETLDVQMGGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSLDYFNTAGLV 300

QY 301 QEAGVLKMTLRDDMIKESKFRLLTKFQFTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 QEAGVLKMTLRDDMIKESKFRLLTKFQFTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELKL 420
DB 361 PTGLTFFPAVDVQAFVLPNSLSASLFLIGHMTTGSMEVSAESNRLVGLKLDRLLELKL 420

QY 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVNVLQPHQNFLLF 480
DB 421 HSNIGPPFVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLNVNVLQPHQNFLLF 480

QY 481 GADVYK 487
DB 481 GADVYK 487
```



```

RESULT 10
US-08-372-783-69
; Sequence 69, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: "rBPI"
;
US-08-372-783-69
Query Match 100.0%; Score 2507; DB 1; Length 487;
Best Local Similarity 100.0%; Pred. No. 6.6e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNFPGVVVRIQKGLDYASQGGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNFPGVVVRIQKGLDYASQGGTAALQKEL 60
Qy 61 KRIKIPDYSDFKIKHLKGHSYFSDMIRFQLPSSQISMVNPVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHSYFSDMIRFQLPSSQISMVNPVGLKFSISNANIKISG 120
Qy 121 KWKAKQKRLKMGNFDLSIEGWSISADLKGNSPTSGKPTITCSCSHINSVHVHISKS 180
Db 121 KWKAKQKRLKMGNFDLSIEGWSISADLKGNSPTSGKPTITCSCSHINSVHVHISKS 180
Qy 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYL 240

Db 181 KVGWLIQLFHKKIESALRNKNNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGLSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGLSDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMIPKESKFRITTKTFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMIPKESKFRITTKTFPGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
Qy 421 HSNIGPPFVELLDIMNYIIVPILVLRVNEKLGKGFPLTPARVQLYNNVILQPHQNFLLF 480
Db 421 HSNIGPPFVELLDIMNYIIVPILVLRVNEKLGKGFPLTPARVQLYNNVILQPHQNFLLF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 11
US-08-372-783-146
; Sequence 146, Application US/08372783
; Patent No. 5578572
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; APPLICANT: Lambert, Lewis H.
; APPLICANT: Little, Roger G.
; TITLE OF INVENTION: Anti-Gram-Positive Bacterial Methods and
; TITLE OF INVENTION: Materials
; NUMBER OF SEQUENCES: 237
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,783
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/273,540
; FILING DATE: 11-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/209,762
; FILING DATE: 11-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/183,222
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/32415
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 146:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: protein
; OTHER INFORMATION: "rBPI"
;
US-08-372-783-146
```

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKEL 60

QY 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISG 120  
DB 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISG 120

QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180

QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDS VAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMVYLGSDYFFNTAGLV 300  
DB 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMVYLGSDYFFNTAGLV 300

QY 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSASNRVLVGLKDLRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSASNRVLVGLKDLRLLELK 420

QY 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVOLYNNVVLQPHQNFLLP 480  
DB 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVOLYNNVVLQPHQNFLLP 480

QY 481 GADVYK 487  
DB 481 GADVYK 487

## RESULT 12

US-08-372-105-69  
; Sequence 69, Application US/08372105  
; Patent No. 5627153  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G.  
; APPLICANT: Lim, Edward  
; APPLICANT: Lambert, Lewis H.  
; APPLICANT: Scannon, Patrick J.  
; TITLE OF INVENTION: Anti-Fungal Materials and Methods  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/372,105  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/273,540  
; FILING DATE: 11-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/209,762

; FILING DATE: 11-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/183,222  
; FILING DATE: 14-JAN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rin-Laures, Li-Hsien  
; REGISTRATION NUMBER: 33,547  
; REFERENCE/DOCKET NUMBER: 27129/32415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 69:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: "FBPI"  
; US-08-372-105-69

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQTAALQKEL 60

QY 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISG 120  
DB 61 KRKIPDYSDFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNVGLKFSISNANIKISG 120

QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180  
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180

QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDS VAGINYL 240

QY 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMVYLGSDYFFNTAGLV 300  
DB 241 VAPPATTAETLDVQMGGEFYSENHNHPPPPAPPVMEFPAADRMVYLGSDYFFNTAGLV 300

QY 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLMKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSASNRVLVGLKDLRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSASNRVLVGLKDLRLLELK 420

QY 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVOLYNNVVLQPHQNFLLP 480  
DB 421 HSNIGPPVVELLDQIMNYIVPILVPRVNEKLGKGFPLTPPARVOLYNNVVLQPHQNFLLP 480

QY 481 GADVYK 487  
DB 481 GADVYK 487

## RESULT 13

US-08-372-105-146  
; Sequence 146, Application US/08372105  
; Patent No. 5627153  
; GENERAL INFORMATION:  
; APPLICANT: Little, Roger G.  
; APPLICANT: Lim, Edward  
; APPLICANT: Lambert, Lewis H.  
; APPLICANT: Scannon, Patrick J.

TITLE OF INVENTION: Anti-Fungal Materials and Methods  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/372,105

FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/273,540

FILING DATE: 11-JUL-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/209,762

FILING DATE: 11-JAN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Rin-Laures Li-Hsien

REGISTRATION NUMBER: 33,547

REFERENCE/DOCKET NUMBER: 27129/32415

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 146:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-372-105-146

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60

Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60

Qy 61 KRKIPDYSDFSFKIKHLGKGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Db 61 KRKIPDYSDFSFKIKHLGKGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAKRFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Db 121 KWKAKRFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLPHKKIESALRNKMSQCEKVTNSVSKLOPYFQTLVPMTKIDSVAGINYL 240

Db 181 KVGWLIQLPHKKIESALRNKMSQCEKVTNSVSKLOPYFQTLVPMTKIDSVAGINYL 240

Qy 241 VAPPATTATETLDVQMGFEYSNHNPPFPAPVMEFPAADHRYVLGLSDYFFNTAGLV 300

Db 241 VAPPATTATETLDVQMGFEYSNHNPPFPAPVMEFPAADHRYVLGLSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMPKESKRLATTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Db 301 YQEAGVLKMTLRDDMPKESKRLATTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMTTGSMEVSAESNRLVGELKLDRLLELK 420

Db 361 PTGLTFYPAVDVQAFVLPNSLASLFLIGMTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPFPVELLDIMNYIVPILVPRVNEKLGKGFPLPTPARVOLXNVVLQPHQNFLLF 480

Db 421 HSNIGPFPVELLDIMNYIVPILVPRVNEKLGKGFPLPTPARVOLXNVVLQPHQNFLLF 480

Qy 481 GADVYK 487

Db 481 GADVYK 487

#### RESULT 14

US-08-415-158-2

Sequence 2, Application US/08415158

Patent No. 5639727

GENERAL INFORMATION:

APPLICANT: Little, Roger G. II

APPLICANT: Gazzano-Santoro, Helene

APPLICANT: Parent, James Brian

TITLE OF INVENTION: Therapeutic uses of

TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein Products

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/415,158

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/093,202

FILING DATE:

APPLICATION NUMBER: US 08/030,644

ATTORNEY/AGENT INFORMATION:

NAME: Sharp, Jeffrey S.

REGISTRATION NUMBER: 31,879

REFERENCE/DOCKET NUMBER: 31580

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-415-158-2

Query Match 100.0%; Score 2507; DB 1; Length 487;

Best Local Similarity 100.0%; Pred. No. 6.6e-209;

Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60

Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRIISQKGLDYASQQGTAALQKEL 60

Qy 61 KRKIPDYSDFSFKIKHLGKGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Db 61 KRKIPDYSDFSFKIKHLGKGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAKRFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Db 121 KWKAKRFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

```
QY      181  KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPVMTKIDSVAGINYL 240
Db      181  KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPVMTKIDSVAGINYL 240
QY      241  VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFNTAGLV 300
Db      241  VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFNTAGLV 300
QY      301  YQAGVULKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360
Db      301  YQAGVULKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360
QY      361  PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361  PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
QY      421  HSNIGPPPVVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480
Db      421  HSNIGPPPVVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480
QY      481  GADVYK 487
Db      481  GADVYK 487

RESULT 15
US-08-064-693-2
; Sequence 2, Application US/08064693
; Patent No. 5643570
; GENERAL INFORMATION:
; APPLICANT: Theofan, Georgia
; APPLICANT: Grinna, Lynn S
; APPLICANT: Horwitz, Arnold
; TITLE OF INVENTION: BPI-Immunoglobulin Fusion Proteins
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064,693
; FILING DATE: 19930519
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers Thomas C.
; REGISTRATION NUMBER: 36,989
; REFERENCE/DOCKET NUMBER: 30659
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-064-693-2
```

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 6.6e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1  MRENMARGPCNAPRWVSLMVLVAIGTAVTAANNPVGWVRISOKGLDYASOQGTAAQLKEL 60
Db      1  MRENMARGPCNAPRWVSLMVLVAIGTAVTAANNPVGWVRISOKGLDYASOQGTAAQLKEL 60
QY      61  KRIRIPDYSDSPKIKHLGKGHYSFYSMDIREFOLPSSQISWPNVGLKFSISNANIKISG 120
Db      61  KRIRIPDYSDSPKIKHLGKGHYSFYSMDIREFOLPSSQISWPNVGLKFSISNANIKISG 120
QY      121  KWKAQKRFKMSGNFPLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180
Db      121  KWKAQKRFKMSGNFPLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKS 180
QY      181  KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPVMTKIDSVAGINYL 240
Db      181  KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPVMTKIDSVAGINYL 240
QY      241  VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGLSDYFNTAGLV 300
Db      241  VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMVYLGLSDYFNTAGLV 300
QY      301  YQAGVULKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360
Db      301  YQAGVULKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360
QY      361  PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361  PTGLTFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLDRLLELK 420
QY      421  HSNIGPPPVVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480
Db      421  HSNIGPPPVVELLDIMNYIVPILVLRVNEKLOKGFPLPTPARVOLYNNVVLQPHQNPLLF 480
QY      481  GADVYK 487
Db      481  GADVYK 487
```

Search completed: October 21, 2005, 11:32:57  
Job time : 49.1759 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:38 ; Search time 64.4411 Seconds  
(without alignments)  
1104.324 Million cell updates/sec

**Title:** US-10-629-516-2 COPY 10 193

Perfect score: 943  
Sequence: 1 CNAPRWVSLMVLVAIGTAVT.....HVHISKSKVGWLIQLFHKKI 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

```
Database : A_Geneseq_16Dec04.*
1: Geneseq1990s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003s.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	943	100.0	220	2	AAR880746	Aar88746 rBPI (1-19
2	943	100.0	221	2	AAR16801	Aaw16801 Recombina
3	943	100.0	230	2	AAM16800	Aaw16800 Recombina
4	943	100.0	230	2	AAR47091	Aaw47091 Human rec
5	943	100.0	243	2	AAR33777	Aar33777 BPIP from
6	943	100.0	243	2	AAM16803	Aaw16803 Recombina
7	943	100.0	267	2	AAM16802	Aaw16802 Recombina
8	943	100.0	300	2	AAM62410	Aaw62410 Bacterici
9	943	100.0	368	2	AAR21840	Aar21840 Human 57k
10	943	100.0	368	2	AAR71291	Aar71291 Human bac
11	943	100.0	483	4	AAB66058	Aab66058 Human Bac
12	943	100.0	483	6	ABO32712	Abo32712 Secreted
13	943	100.0	483	6	ABO04504	Abu04504 Human exp
14	943	100.0	483	6	ABU04575	Abu04575 Human exp
15	943	100.0	483	8	ADQ10386	Adq10386 Human pol
16	943	100.0	483	8	ADQ98258	Adq98258 Human pol
17	943	100.0	487	1	AAU06198	Aau06198 Human bac
18	943	100.0	487	2	AAR24777	Aar24777 Sequence
19	943	100.0	487	2	AAR44420	Aar44420 pING4512
20	943	100.0	487	2	AAR43886	Aar43886 Human bac
21	943	100.0	487	2	AAR62370	Aar62370 Recombina
22	943	100.0	487	2	AAR57901	Aar57901 Bacterici
23	943	100.0	487	2	AAR62344	Aar62344 Recombina
24	943	100.0	487	2	AAR68923	Aar68923 Bacterici
25	943	100.0	487	2	AAR71290	Aar71290 Human bac

## ALIGNMENTS

## RESULT 1

REC'D  
AAR88746  
ID AAR88746 standard; protein: 220 AA.

AA  
AC AAR88746;

DT 10-APR-1996 (first entry)

DE RBPI(1-193) with 27 amino acid signal peptide.

AA bactericidal-permeability increasing protein; BPI; truncated; dimer;  
KW  
KW  
KW endotoxic shock; heparin neutralisation; angiogenesis; inhibitor; ss.  
AA

XX OS Synthetic.

XX	Key	Location/Qualifiers
FH	Peptide	1. .27
FT		1. .27

```

F1
FT
FT
FT

```

FT	Protein	Repeats
FT		28. .220

FT  
1000000  
/label= rBPI(1-193)

/note= "the first 193 residues of human mature BPI"

US5447913-A.

05-SEP-1995

XX  
PE 11-MAR-1994: 94IIS-00212132-XX  
PR 11-MAR-1994: 94US-00212132.XX  
PA (XOMA ) XOMA CORP.XX  
PT  
Ammons WS. Little BG:

XX  
DP WPT: 1995-319904/41

XX Improved use of a bactericidal permeability increasing protein - for  
PT neutralisation of heparin and treatment of endo-toxaemia, by admin. of  
PT covalently linked dimer of N-terminal fragment.

XX  
PS  
Example 1: Page 2: 36pp: English:

Compositions of N-terminal fragments (i.e. amino acids 1-193 to 1-199) of human bactericidal-permeability increasing (BPI) protein are used to neutralise heparin and to treat endotoxaemia. Efficacy of such compounds is improved when they comprise at least 50% of the truncated rBPI in

CC dimeric form. The present sequence is that of rBPI(1-193) in which the  
 CC first 4 amino acids of the BPI signal peptide are removed; the codon  
 CC specifying the fifth amino acid of the signal sequence (Met at position -  
 CC 27) is placed in the context of a consensus Kozak translation initiation  
 CC sequence. This truncated rBPI is the preferred monomer for dimerisation  
 CC in the presence of copper 2+ ions. N.B. The patent specification includes  
 CC the known full-length BPI sequence but does not contain sequences for any  
 CC of the truncated versions of the protein. The present sequence has been  
 CC obtained by modifying the wild-type sequence according to the description  
 CC given by the inventors  
 XX  
 SQ Sequence 220 AA;

Query Match 100.0%; Score 943; DB 2; Length 220;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60  
 DB 6 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 65  
 QY 61 DSFKIKHLGKGHYSFYSMDIREQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
 DB 66 DSFKIKHLGKGHYSFYSMDIREQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 125  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180  
 DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 185  
 QY 181 HKKI 184  
 DB 186 HKKI 189

RESULT 2  
 ID AAW16801 standard; protein; 221 AA.  
 XX AAW16801;  
 XX  
 DT 28-JUL-1997 (first entry)  
 XX  
 DE Recombinant endotoxin neutralising polypeptide Lot #159699.  
 XX  
 KW Recombinant; endotoxin; neutralisation; RNP; Lot #159699;  
 KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;  
 KW detection; Gram-negative; bacterium; infection; prevention; treatment;  
 KW disorder; mediation; stimulation; neutrophil; mononuclear cell;  
 KW inhibition; shock; anaemia; anaemia;  
 KW disseminated intravascular coagulation; thrombocytopenia;  
 KW thrombocytopaenia; adult respiratory distress syndrome; ARDS;  
 KW renal failure; liver disease; half life; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Peptide 1. .31  
 FT /label= sig\_peptide  
 XX  
 PN WO9634873-A1.  
 XX  
 PD 07-NOV-1996.  
 XX  
 XX 01-MAY-1996; 96WO-US006134.  
 XX  
 XX 01-MAY-1995; 95US-00431517.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 PI Scott RW, Marra MN;  
 XX  
 XX WPI; 1996-506090/50.  
 DR

XX  
 PT Lipo.polysaccharide binding and endotoxin neutralising polypeptide -  
 PT useful in diagnosis, prevention and treatment of Gram-negative bacterial  
 PT infection and associated disorders and conditions.  
 XX  
 PS Example 1; Page: 147pp; English.

XX  
 CC The present sequence is the recombinant endotoxin neutralising  
 CC polypeptide (RNP) B(1-190) (Lot #159699), which comprises residues 1-190  
 CC of human bactericidal/permeability increasing protein (hBPI). The RNP,  
 CC which selectively and specifically binds lipopolysaccharide (LPS) and has  
 CC endotoxin neutralising activity, can be used to detect a site of Gram  
 CC negative bacterial infection, and prevent or treat endotoxin related  
 CC disorders, preferably where LPS mediated stimulation of neutrophils and  
 CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular  
 CC coagulation, anaemia, thrombocytopaenia, adult respiratory distress  
 CC syndrome, renal failure, liver disease and conditions associated with  
 CC Gram negative bacterial infection. The RNP has an enhanced serum half  
 CC life relative to naturally occurring BPI, and binds LPS without  
 CC triggering a significant, undesirable immune response. N.B. Sequence not  
 CC given in specification, but produced using the wild type hBPI sequence  
 CC given in figure 3  
 XX  
 SQ Sequence 221 AA;

Query Match 100.0%; Score 943; DB 2; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLGKGHYSFYSMDIREQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
 DB 70 DSFKIKHLGKGHYSFYSMDIREQLPSSQISMPVNVGLKFSISNANIKISGKWKAKRFL 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 180  
 DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLF 189  
 QY 181 HKKI 184  
 DB 190 HKKI 193

RESULT 3  
 ID AAW16800 standard; protein; 230 AA.  
 XX AAW16800;  
 AC AAW16800;  
 XX  
 DT 28-JUL-1997 (first entry)  
 XX  
 DE Recombinant endotoxin neutralising polypeptide NCY108.  
 XX  
 KW Recombinant; endotoxin; neutralisation; RNP; NCY108; lipopolysaccharide;  
 KW LPS; bactericidal; permeability; increase; BPI; detection; Gram-negative;  
 KW bacterium; infection; prevention; treatment; disorder; mediation;  
 KW stimulation; neutrophil; mononuclear cell; inhibition; shock; anaemia;  
 KW anaemia; disseminated intravascular coagulation; thrombocytopenia;  
 KW thrombocytopaenia; adult respiratory distress syndrome; ARDS;  
 KW renal failure; liver disease; half life; human.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1. .31  
 FT /label= sig\_peptide  
 XX  
 PN WO9634873-A1.

PD 07-NOV-1996.  
 XX  
 XX  
 XX 01-MAY-1996; 96WO-US006134.  
 XX  
 XX 01-MAY-1995; 95US-00431517.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 XX  
 XX Scott RW, Marra MN;  
 XX  
 XX WPI; 1996-506090/50.  
 DR  
 XX  
 XX Lipo:polysaccharide binding and endotoxin neutralising polypeptide -  
 PT useful in diagnosis, prevention and treatment of Gram-negative bacterial  
 PT infection and associated disorders and conditions.  
 PT  
 XX  
 XX Example 1; Page; 147pp; English.  
 PS  
 XX  
 XX The present sequence is the recombinant endotoxin neutralising  
 CC polypeptide (RENIP) B(1-199) (NCY108), which comprises residues 1-199 of  
 CC human bactericidal/permeability increasing protein (hBPI). The RENIP,  
 CC which selectively and specifically binds lipopolysaccharide (LPS) and has  
 CC endotoxin neutralising activity, can be used to detect a site of Gram  
 CC negative bacterial infection, and prevent or treat endotoxin related  
 CC disorders, preferably where LPS mediated stimulation of neutrophils and  
 CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular  
 CC coagulation, anaemia, thrombocytopenia, adult respiratory distress  
 CC syndrome, renal failure, liver disease and conditions associated with  
 CC Gram negative bacterial infection. The RENIP has an enhanced serum half  
 CC life relative to naturally occurring BPI, and binds LPS without  
 CC triggering a significant, undesirable immune response. N.B. Sequence not  
 CC given in specification, but produced using the wild type hBPI sequence  
 CC given in figure 3  
 XX  
 XX Sequence 230 AA;  
 SQ  
 Query Match 100.0%; Score 943; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPVGVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPVGVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLKGHYFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLKGHYFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180  
 DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 189  
 QY 181 HKKI 184  
 DB 190 HKKI 193  
 RESULT 4  
 AAW47091  
 ID AAW47091 standard; protein; 230 AA.  
 XX  
 AC AAW47091;  
 XX  
 DT 18-MAY-1998 (first entry)  
 XX  
 DE Human recombinant BPI (rBPI23) protein.  
 XX  
 KW Bactericidal/permeability increasing protein; BPI; clot formation; TA;  
 KW clot dissolution; thrombosis; thrombolytic agent; recombinant.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT Peptide 1..31  
 FT /note= "signal sequence"  
 FT Protein 32..230  
 FT /note= "mature recombinant rBPI23 protein"  
 FT Misc-difference 216  
 FT /label= K216E  
 FT /note= "wild-type Lys is replaced by Glu"  
 XX  
 XX WO9742967-A1.  
 XX  
 XX 20-NOV-1997.  
 XX  
 XX 09-MAY-1997; 97WO-US008017.  
 XX  
 XX 10-MAY-1996; 96US-00644290.  
 XX  
 XX (XOMA ) XOMA CORP.  
 XX  
 XX White ML, Ammons WS;  
 XX  
 XX WPI; 1998-008579/01.  
 XX  
 XX N-PSDB; AAV13962.  
 XX  
 XX Use of bactericidal/permeability-increasing protein products - for  
 PT slowing clot formation and enhancing clot dissolution in blood,  
 PT particularly for treating thrombotic disorders.  
 XX  
 XX Example 1; Page; 56pp; English.  
 XX  
 XX This is a recombinant bactericidal/permeability-increasing (BPI) protein  
 CC product rBPI23. A BPI protein product can be administered especially by  
 CC contacting with blood to delay or prevent clot formation in the blood or  
 CC to enhance clot dissolution in the blood. A BPI protein product can also  
 CC be administered, optionally with a thrombolytic agent (TA), to treat a  
 CC patient suffering from thrombotic disorders such as arterial thrombosis,  
 CC coronary artery thrombosis, myocardial infarction, cerebral artery  
 CC thrombosis or occlusion, intracardiac thrombosis, peripheral arterial  
 CC thrombosis associated with exposure of blood to a foreign or injured  
 CC tissue surface, hypercoagulability, non-endotoxin-associated  
 CC coagulopathies, and non-endotoxin-associated disseminated intravascular  
 CC coagulopathy. The BPI protein products can be used in a method for  
 CC enhancing reperfusion or reducing reocclusion in a subject treated with a  
 CC TA comprising co-administration of the BPI protein product and the TA and  
 CC in a method for decreasing the dose of a TA required to establish  
 CC reperfusion or to reduce reocclusion in a subject comprising co-  
 CC administration of a BPI protein product and a TA, the dosage of the TA  
 CC being less than that required for a desired pharmaceutical effect when  
 CC the TA is administered as a monotherapy. The BPI protein products have  
 CC anticoagulant and thrombolytic activity and can be used for the  
 CC prophylactic and therapeutic treatment of thrombotic disorders. The BPI  
 CC products can be used to reduce the dosage of antithrombotic agent  
 CC required, thereby reducing or eliminating potential side effects. Note:  
 CC This sequence is not provided in the specification. It has been created  
 CC by modifying the natural BPI protein sequence given in Pages 46-48 of the  
 CC specification  
 XX  
 XX Sequence 230 AA;  
 SQ  
 Query Match 100.0%; Score 943; DB 2; Length 230;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPVGVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
 DB 10 CNAPRWVSLMVLVAIGTAVTAANPVGVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLKGHYFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLKGHYFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180

```
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 5
AAR33777
AC AAR33777;
DT 25-MAR-2003 (revised)
DT 22-JUL-1993 (first entry)
XX BPIP from p212.
XX Bacterial/permeability increasing protein; lipopolysaccharide; LPS;
KW inhibitor; endotoxin-related shock;
KW disseminated intravascular coagulation; anaemia; thrombocytopenia; ARDS;
KW renal failure; endotoxaemia; adult respiratory distress syndrome.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..32 "signal peptide"
FT Region 32..243
FT /note= "mature protein"
XX WO9305797-A1.
XX 01-APR-1993.
XX 28-SEP-1992; 92WO-US008234.
XX 27-SEP-1991; 91US-00766566.
XX (INCY-) INCYTE PHARM INC.
XX Marra MN, Scott RW, Snable JL, Wilde CG;
XX WPI; 1993-117241/14.
XX Compens. contg. a bactericidal and permeability increasing protein -
XX solubilised in a lipid carrier to maintain stably an active form.
XX Disclosure; Fig 7; 53pp; English.
XX The human bactericidal/permeability increasing protein may be used in a
XX compsn. solubilised in a lipid carrier. The BPIP binds
XX lipopolysaccharides and inhibits the immunostimulatory and toxic
XX activities of LPS in vitro and in vivo. The lipid compsn. stably
XX maintains the BPIP in a sol. active form. The compsn. can be used for
XX detecting or quantifying LPS in a sample, coating a surgical tool,
XX coating an implantable invasive device, decontaminating a fluid contg.
XX LPC and treating endotoxin related -shock, -disseminated intravascular
XX coagulation, -anaemia, -thrombocytopenia, -adult respiratory stress
XX syndrome or -renal failure, or for preventing endotoxaemia. See also
XX AAR33776, AAR33729-31. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 243 AA;
Qy Query Match 100.0%; Score 943; DB 2; Length 243;
Db Best Local Similarity 100.0%; Pred. No. 1.6e-92;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CNAPRWLSMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 60
Db 10 CNAPRWLSMLVLAIGTAVTAANVPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 69
```

```
Qy 61 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKPSISNANIKISGKWAQKRFL 120
Db 70 DSFKIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKPSISNANIKISGKWAQKRFL 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 6
AAW16803
ID AAW16803 standard; protein; 243 AA.
XX AAW16803;
XX 28-JUL-1997 (first entry)
XX Recombinant endotoxin neutralising polypeptide Lot #159693.
DE Recombinant; endotoxin; neutralisation; RENP; Lot #159693;
KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;
KW detection; Gram-negative; bacterium; infection; prevention; treatment;
KW disorder; mediation; stimulation; neutrophil; mononuclear cell;
KW inhibition; shock; anemia; anaemia;
KW disseminated intravascular coagulation; thrombocytopenia;
KW thrombocytopenia; adult respiratory distress syndrome; ARDS;
KW renal failure; liver disease; half life; human.
XX Homo sapiens.
XX Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..31
FT /label= sig_peptide
XX WO9634873-A1.
XX 07-NOV-1996.
XX 01-MAY-1996; 96WO-US006134.
XX 01-MAY-1995; 95US-00431517.
XX (INCY-) INCYTE PHARM INC.
XX Scott RW, Marra MN;
XX WPI; 1996-506090/50.
XX Lipo:polysaccharide binding and endotoxin neutralising polypeptide -
XX useful in diagnosis, prevention and treatment of Gram-negative bacterial
XX infection and associated disorders and conditions.
XX Example 1; Page; 147pp; English.
XX The present sequence is the recombinant endotoxin neutralising
XX polypeptide (RENP) B(1-212) (Lot #159693), which comprises residues 1-212
XX of human bactericidal/permeability increasing protein (hBPI). The RENP,
XX which selectively and specifically binds lipopolysaccharide (LPS) and has
XX endotoxin neutralising activity, can be used to detect a site of Gram
XX negative bacterial infection, and prevent or treat endotoxin related
XX disorders, preferably where LPS mediated stimulation of neutrophils and
XX mononuclear cells is inhibited, e.g. shock, disseminated intravascular
XX coagulation, anaemia, thrombocytopenia, adult respiratory distress
XX syndrome, renal failure, liver disease and conditions associated with
XX Gram negative bacterial infection. The RENP has an enhanced serum half
XX life relative to naturally occurring BPI, and binds LPS without
XX triggering a significant, undesirable immune response. N.B. Sequence not
XX given in specification, but produced using the wild type hBPI sequence
```



```
CC given in figure 3
XX Sequence 243 AA;
SQ
    Query Match      100.0%; Score 943; DB 2; Length 243;
    Best Local Similarity 100.0%; Pred. No. 1.8e-92;
    Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69
Qy 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 120
Db 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 129
Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHLSKSVGWLIOLF 180
Db 130 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHLSKSVGWLIOLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 7
AAW16802
ID AAW16802 standard; protein; 267 AA.
XX
AC AAW16802;
XX
DT 28-JUL-1997 (first entry)
XX
DE Recombinant endotoxin neutralising polypeptide Lot #159695.
XX
KW Recombinant; endotoxin; neutralisation; REMP; Lot #159695;
KW lipopolysaccharide; LPS; bactericidal; permeability; increase; BPI;
KW detection; Gram-negative; bacterium; infection; prevention; treatment;
KW disorder; mediation; stimulation; neutrophil; mononuclear cell;
KW inhibition; shock; anaemia; anaemia;
KW disseminated intravascular coagulation; thrombocytopenia;
KW thrombocytopenia; adult respiratory distress syndrome; ARDS;
KW renal failure; liver disease; half life; human.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= sig_peptide
XX
FN WO9634873-A1.
XX
PD 07-NOV-1996.
XX
PF 01-MAY-1996; 96WO-US006134.
XX
PR 01-MAY-1995; 95US-00431517.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Scott RW, Marra MN;
XX
XX WPI; 1996-506090/50.
XX
XX Lipo:polysaccharide binding and endotoxin neutralising polypeptide -
XX useful in diagnosis, prevention and treatment of Gram-negative bacterial
XX infection and associated disorders and conditions.
XX
XX Example 1; Page; 147pp; English.
XX
XX The present sequence is the recombinant endotoxin neutralising
XX polypeptide (RENP) B(1-236) (Lot #159695), which comprises residues 1-236
CC
```

```
CC of human bactericidal/permeability increasing protein (hBPI). The RENP,
CC which selectively and specifically binds lipopolysaccharide (LPS) and has
CC endotoxin neutralising activity, can be used to detect a site of Gram
CC negative bacterial infection, and prevent or treat endotoxin related
CC disorders, preferably where LPS mediated stimulation of neutrophils and
CC mononuclear cells is inhibited, e.g. shock, disseminated intravascular
CC coagulation, anaemia, thrombocytopenia, adult respiratory distress
CC syndrome, renal failure, liver disease and conditions associated with
CC Gram negative bacterial infection. The RENP has an enhanced serum half
CC life relative to naturally occurring BPI, and binds LPS without
CC triggering a significant, undesirable immune response. N.B. Sequence not
CC given in specification, but produced using the wild type hBPI sequence
CC given in figure 3
XX
SQ Sequence 267 AA;
    Query Match      100.0%; Score 943; DB 2; Length 267;
    Best Local Similarity 100.0%; Pred. No. 1.8e-92;
    Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 60
Db 10 CNAPRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGGTAALQKELKRIKIPDYS 69
Qy 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 120
Db 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQKRF 129
Qy 121 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHLSKSVGWLIOLF 180
Db 130 KMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHLSKSVGWLIOLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 8
AAW62410
ID AAW62410 standard; protein; 300 AA.
XX
AC AAW62410;
XX
DT 01-OCT-1998 (first entry)
XX
DE Bactericidal permeability increasing factor #1.
XX
KW Bactericidal; Pseudomonas sp; endotoxin shock; bacterial infection;
KW bactericidal permeability increasing factor; B/P1; neutralising;
KW human neutrophil granule bactericidal protein.
XX
OS Homo sapiens.
XX
FN US5786324-A.
XX
PD 28-JUL-1998.
XX
PF 24-MAR-1994; 94US-00218026.
XX
PR 24-MAR-1994; 94US-00218026.
XX
XX (MINU) UNIV MINNESOTA.
XX
XX Mayo K, Haseman JR, Gray B;
XX
XX WPI; 1998-436578/37.
XX
XX N-PSDB; AAY39860.
XX
XX Bactericidal and endotoxin-neutralising peptides - used in treating e.g.
XX Pseudomonas species infection and in protectively coating prosthetic
XX devices.
XX
XX Example 1; Fig 4; 46pp; English.
PS
```



CC p337 protein is a 38 kDa non-glycosylated variant of human bactericidal-  
 CC permeability increasing protein (see AAR71290), which has antibacterial  
 CC activity against Gram-negative bacteria, inhibits lipopolysaccharide  
 CC (LPS) directly, and inhibits LPS-mediated tumor necrosis factor  
 CC production from mononuclear cells. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 CC  
 XX Sequence 368 AA;  
 SQ  
 Query Match 100.0%; Score 943; DB 2; Length 368;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-92; Mismatches 0; Indels 0; Gaps 0;  
 Matches 184; Conservative 0;  
 QY 1 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60  
 DB 10 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 69  
 QY 61 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 70 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 129  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180  
 DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 189  
 QY 181 HKKI 184  
 DB 190 HKKI 193  
 RESULT 11  
 AAB66058  
 ID AAB66058 standard; protein; 483 AA.  
 XX  
 AC AAB66058;  
 XX  
 DT 30-MAR-2001 (first entry)  
 XX  
 DE Human Bactericidal Permeability Increasing, BPI protein.  
 XX  
 KW Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder;  
 KW central nervous system; focal brain disorder; bipolar affective disorder;  
 KW global-diffuse cerebral disorder; cerebrovascular; Alzheimer's disease;  
 KW senile dementia; Huntington's disease; amyotrophic lateral sclerosis;  
 KW Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;  
 KW neuropsychiatric; psychoactive substance use; anxiety.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200077239-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 24-MAY-2000; 2000WO-US014859.  
 XX  
 PR 14-JUN-1999; 99US-00333159.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI McCarthy SA, Fraser CC, Sharp JD, Barnes TM;  
 XX  
 DR WPI; 2001-032313/04.  
 XX  
 PT TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for  
 PT screening assays and diagnostic assays and for the treatment of  
 PT neurological diseases such as Alzheimer's, Parkinson's and Huntington's  
 PT disease.  
 XX  
 PS Claim 8; Fig 5; 359pp; English.  
 XX  
 CC The present invention relates to TANGO or INTERCEPT proteins and coding  
 CC sequences (see AAF45121-F45136 and AAF45138-F45139 and AAB66031-B66057,  
 CC AAB66064-B66083 and AAB66085). The TANGO/INTERCEPT proteins and coding

CC sequences are useful for the treatment of neurological disorders such as  
 CC central nervous system (CNS) disorders, CNS-related disorders, focal  
 CC brain disorders, global-diffuse cerebral disorders and other neurological  
 CC and cerebrovascular disorders. The CNS disorders include Alzheimer's  
 CC disease, senile dementia, Huntington's disease, amyotrophic lateral  
 CC sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autonomic  
 CC function disorders such as hypertension and sleep disorders,  
 CC neuropsychiatric disorders, psychoactive substance use disorders,  
 CC anxiety, and bipolar affective disorder. The present sequence is a  
 CC sequence used in a sequence homology alignment with the TANGO/INTERCEPT  
 CC sequences of the present invention  
 XX  
 SQ Sequence 483 AA;  
 Query Match 100.0%; Score 943; DB 4; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 60  
 DB 6 CNAFRWVSLMVLVAIGTAVTAAVNPVGVVVRISQKGLDYASQGTAAALQKELKRIKIPDYS 65  
 QY 61 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 120  
 DB 66 DSFKIKHLGKGHYSPYSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRF 125  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 180  
 DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKVGVWLIQLF 185  
 QY 181 HKKI 184  
 DB 186 HKKI 189  
 RESULT 12  
 ABO32712  
 ID ABO32712 standard; protein; 483 AA.  
 XX  
 AC ABO32712;  
 XX  
 DT 17-SEP-2003 (first entry)  
 XX  
 DE Secreted polypeptide-related protein #90.  
 XX  
 KW Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;  
 KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;  
 KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;  
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;  
 KW myocardial infarction; congestive heart disease; blood platelet disorder;  
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US200302279-A1.  
 XX  
 PD 30-JAN-2003.  
 XX  
 PF 12-JAN-2001; 2001US-00759130.  
 XX  
 PR 14-JUN-1999; 99US-00333159.  
 PR 29-JUN-1999; 99US-00342364.  
 PR 10-SEP-1999; 99US-00393996.  
 PR 19-OCT-1999; 99US-00420707.  
 PR 07-JAN-2000; 2000US-00479249.  
 PR 27-APR-2000; 2000US-00559497.  
 PR 24-MAY-2000; 2000US-00578063.  
 PR 16-JUN-2000; 2000US-00596194.  
 PR 23-JUN-2000; 2000US-00602871.  
 PR 30-JUN-2000; 2000US-00608452.  
 XX  
 XX (FRAS/) FRASER C C.  
 PA (BARN/) BARNES T M.

PA (SHARP) SHARP J D.  
 PA (KIRST) KIRST S J.  
 PA (MYER) MYERS P S.  
 PA (LEIB) LEIBY K R.  
 PA (HOLT) HOLTZMAN D A.  
 PA (MCCA) MCCARTHY S A.  
 PA (WRIG) WRIGHTON N.  
 PA (WACK) WACKAY C R.  
 PA (GOOD) GOODEARL A D J.  
 XX  
 PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;  
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
 XX  
 XX WPI: 2003-456290/43.  
 XX  
 XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,  
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in  
 PT forensic biology.  
 XX  
 XX Claim 9; Fig 28F-28G; 482pp; English.  
 XX  
 XX The invention relates to secreted polypeptide-related proteins and  
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The  
 CC nucleic acids, proteins and antibodies specific to the proteins are  
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and  
 CC prophylactic and therapeutic methods. The sequences are used in  
 CC diagnosing, preventing or treating proliferative disorders (e.g.  
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders  
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood  
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
 CC acids may also be used in chromosome mapping, tissue typing and forensic  
 CC biology, and as surrogate markers. This sequence represents a secreted  
 CC polypeptide-related protein of the invention. Note: The sequence data for  
 CC this patent was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 483 AA;

Query Match 100.0%; Score 943; DB 6; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
 DB 6 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65  
 QY 61 DSFKIKHLGKHGHSFYFYSMDIREFOLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120  
 DB 66 DSPKIKHLGKHGHSFYFYSMDIREFOLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 125  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHINSVHVHISKVGWLIQLF 180  
 DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHINSVHVHISKVGWLIQLF 185  
 QY 181 HKKI 184  
 DB 186 HKKI 189  
 RESULT 13  
 ID ABU04504  
 ID ABU04504 standard; protein; 483 AA.  
 XX  
 AC ABU04504;  
 XX  
 DT 29--JAN-2003 (first entry)  
 XX  
 XX Human expressed protein tag (EPT) #1170.

XX  
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
 KW protease; protease inhibitor; transporter; cytoskeletal protein;  
 KW receptor; transcription factor; cancer; MHC;  
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200278524-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 XX 28-MAR-2002; 2002WO-US009671.  
 XX  
 XX 28-MAR-2001; 2001US-0279495P.  
 PR 21-MAY-2001; 2001US-0292544P.  
 PR 08-AUG-2001; 2001US-0310801P.  
 PR 01-OCT-2001; 2001US-0326370P.  
 PR 04-DEC-2001; 2001US-0336780P.  
 PR 20-FEB-2002; 2002US-0358985P.  
 XX  
 XX (ZYCO-) ZYCOS INC.  
 PA  
 XX Chicx RM, Tomlinson AJ, Urban RG;  
 PI  
 XX WPI: 2003-040607/03.  
 XX  
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
 PT cytoskeletal proteins, receptors or transcription factors), useful for  
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
 PT leukemia.  
 PT  
 XX Example 2; SEQ ID NO 1170; 134pp; English.  
 XX  
 XX The invention describes a purified polypeptide, which comprises a  
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
 CC transporter, cytoskeletal protein, receptor or transcription factor. The  
 CC polypeptide is useful as an immunogenic composition for eliciting in a  
 CC mammal an immunogenic response directed against any of the purified  
 CC polypeptide, is useful for treating cancer. The polypeptide is also  
 CC useful for identifying compounds that binds to a naturally processed  
 CC class I or class II MHC-binding polypeptide. The polypeptides and  
 CC polynucleotides are particularly useful for treating or preventing  
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
 CC lymphoma or leukaemia. These are also useful for screening agents for  
 CC treating the above mentioned diseases. This sequence represents an  
 CC expressed protein tag (EPT) isolated from human tissue for translational  
 CC profiling. Note: This sequence does not appear in the printed  
 CC specification but was obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 483 AA;  
 Query Match 100.0%; Score 943; DB 6; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-92;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60  
 DB 6 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65  
 QY 61 DSFKIKHLGKHGHSFYFYSMDIREFOLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 120  
 DB 66 DSPKIKHLGKHGHSFYFYSMDIREFOLPSSQISMPNVGLKFSISNANIKISGKWKAKRFL 125  
 QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHINSVHVHISKVGWLIQLF 180  
 DB 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHINSVHVHISKVGWLIQLF 185  
 QY 181 HKKI 184  
 DB 186 HKKI 189

Db 186 HKKI 189

RESULT 14  
ABU04575

ID ABU04575 standard; protein; 483 AA.

XX AC ABU04575;

XX DT 29-JAN-2003 (first entry)

XX DE Human expressed protein tag (EPT) #1241.

XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;  
KW protease; protease inhibitor; transporter; cytoskeletal protein;  
KW receptor; transcription factor; cancer; MHC;  
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;  
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX OS Homo sapiens.

XX PN WO200278524-A2.

XX PD 10-OCT-2002.

XX PF 28-MAR-2002; 2002WO-US009671.

XX PR 28-MAR-2001; 2001US-0279495P.

XX PR 21-MAY-2001; 2001US-0292544P.

XX PR 08-AUG-2001; 2001US-0310801P.

XX PR 01-OCT-2001; 2001US-0326370P.

XX PR 04-DEC-2001; 2001US-0336780P.

XX PR 20-FEB-2002; 2002US-0358985P.

XX PA (ZYCO-) ZYCOS INC.

XX PI Chicx RM, Tomlinson AJ, Urban RG;

XX DR WPI; 2003-040607/03.

XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,  
PT cytoskeletal proteins, receptors or transcription factors), useful for  
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or  
PT leukemia.

XX PS Example 2; SEQ ID NO 1241; 134pp; English.

XX CC The invention describes a purified polypeptide, which comprises a  
CC fragment of a kinase, phosphatase, protease, protease inhibitor,  
CC transporter, cytoskeletal protein, receptor or transcription factor. The  
CC polypeptide is useful as an immunogenic composition for eliciting in a  
CC mammal an immunogenic response directed against any of the purified  
CC polypeptide. The purified polypeptide, or the antibody that binds to this  
CC polypeptide, is useful for treating cancer. The polypeptide is also  
CC useful for identifying compounds that binds to a naturally processed  
CC class I or class II MHC-binding polypeptide. The polypeptides and  
CC polynucleotides are particularly useful for treating or preventing  
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,  
CC lymphoma or leukaemia. These are also useful for screening agents for  
CC treating the above mentioned diseases. This sequence represents an  
CC expressed protein tag (EPT) isolated from human tissue for translational  
CC profiling. Note: This sequence does not appear in the printed  
CC specification but was obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 483 AA;

Query Match 100.0%; Score 943; DB 6; Length 483;  
Best Local Similarity 100.0%; Pred. No. 4, 1e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 60  
|||||

Db 6 CNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 65

Qy 61 DSFKIKHLGKHGHSFYSDIREFOLPSSQISWVNVGLKPSISNANIKISGKWAQKRFL 120  
|||||

Db 66 DSFKIKHLGKHGHSFYSDIREFOLPSSQISWVNVGLKPSISNANIKISGKWAQKRFL 125  
|||||

Qy 121 KWSGNFDLSIRGMSISADLKLGSNPTSGKPTTITCSSSSHNSVHVHISKSKVGLIOLF 180  
|||||

Db 126 KWSGNFDLSIRGMSISADLKLGSNPTSGKPTTITCSSSSHNSVHVHISKSKVGLIOLF 185  
|||||

Qy 181 HKKI 184  
|||||

Db 186 HKKI 189

RESULT 15  
ADQ10386

ID ADQ10386 standard; protein; 483 AA.

XX AC ADQ10386;

XX DT 09-SEP-2004 (first entry)

XX DE Human polypeptide #206.

XX KW Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;  
KW anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;  
KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;  
KW arteriosclerosis; hypertension; bacterial infection; psoriasis;  
KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;  
KW Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;  
KW goiter; infertility; endometriosis; muscular disorder.

XX OS Homo sapiens.

XX PN US2004121396-A1.

XX PD 24-JUN-2004.

XX PF 19-DEC-2003; 2003US-00741790.

XX PR 14-JUN-1999; 99US-00333159.

XX PR 29-JUN-1999; 99US-00342364.

XX PR 10-SEP-1999; 99US-00393996.

XX PR 19-OCT-1999; 99US-00420707.

XX PR 07-JAN-2000; 2000US-00479249.

XX PR 27-APR-2000; 2000US-00559497.

XX PR 24-MAY-2000; 2000US-00578063.

XX PR 16-JUN-2000; 2000US-00596194.

XX PR 23-JUN-2000; 2000US-00602871.

XX PR 30-JUN-2000; 2000US-00608452.

XX PR 12-JAN-2001; 2001US-00759130.

XX (MILL-) MILLENNIUM PHARM INC.

XX PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;  
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
XX WPI; 2004-479675/45.

XX DR New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and  
XX treating cancer, constipation, hemorrhoids, cystic fibrosis,  
PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,  
PT tuberculosis, malaria, goiter, infertility.

XX PS Claim 9; SEQ ID NO 408; 483pp; English.

XX CC The invention relates to human polynucleotides and the polypeptides they  
CC encode. The invention also relates to a host cell containing a  
CC polynucleotide of the invention, an antibody which selectively binds with  
CC a polypeptide of the invention, a method of detecting the presence of a  
CC polypeptide in a sample, a method of identifying a compound which binds  
CC with a polypeptide, and a method of modulating the activity of a

CC polypeptide. The polynucleotides, polypeptides and compositions are  
CC useful for diagnosing, preventing and/or treating cancer, obesity, host  
CC gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host  
CC reactions, allergic reactions, cystic fibrosis, hypogonadism,  
CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,  
CC hypertension, bacterial infections, psoriasis, diabetes mellitus,  
CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's  
CC disease, AIDS, tuberculosis, viral infections, malaria, goiter,  
CC infertility, endometriosis, wounds and muscular disorders. This sequence  
CC represents a human polypeptide of the invention. Note: The sequence data  
CC for this patent did not form part of the printed specification but was  
CC obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 483 AA;  
  
Query Match 100.0%; Score 943; DB 8; Length 483;  
Best Local Similarity 100.0%; Pred. No. 4,1e-92;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CNAPRWVSLMVLVAIGTAVTAAVNPVGWVVRISQKGLDYASQOGTAALQKELKIKIPDYS 60  
Db |||||  
6 CNAPRWVSLMVLVAIGTAVTAAVNPVGWVVRISQKGLDYASQOGTAALQKELKIKIPDYS 65  
Qy 61 DSPKIKHLGKGHSFYSGMDIREFQPSQISMPVNVGLKFSISNANIKISGKWKAKRFL 120  
Db |||||  
66 DSPKIKHLGKGHSFYSGMDIREFQPSQISMPVNVGLKFSISNANIKISGKWKAKRFL 125  
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 180  
Db |||||  
126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF 185  
Qy 181 HKKI 184  
Db ||||  
186 HKKI 189

Search completed: October 21, 2005, 11:26:47  
Job time : 65.4411 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM'protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 37.7407 Seconds  
(without alignments)  
1241.566 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQPHQNFLLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2507	100.0	487	A30909	bactericidal/perme
2	1627.5	64.9	482	S10180	bactericidal/perme
3	1288	51.4	250	S43383	bactericidal/perme
4	1087	43.4	481	A54136	lipopolysaccharide
5	1052	42.0	477	A35843	lipopolysaccharide
6	1039	41.4	481	I56246	lipopolysaccharide
7	985.5	39.3	482	B35843	lipopolysaccharide
8	465	18.5	493	A53533	phospholipid trans
9	463.5	18.5	493	I43370	plasma phospholipi
10	337.5	13.5	488	C86183	hypothetical prote
11	295	11.8	493	A26941	cholesteryl ester
12	282	11.2	493	A53176	cholesteryl ester
13	271.5	10.8	497	I46692	cholesteryl ester
14	261.5	10.4	470	S17447	probable ligand-bi
15	234.5	9.4	473	S17448	probable ligand-bi
16	222	8.9	606	T29190	hypothetical prote
17	205.5	8.2	487	T18952	hypothetical prote
18	189	7.5	464	T16889	hypothetical prote
19	186.5	7.4	486	T20482	hypothetical prote
20	175	7.0	554	T15438	hypothetical prote
21	174	6.9	576	T22700	hypothetical prote
22	154	6.1	824	E87856	protein F10D11.6 [
23	154	6.1	846	T20710	hypothetical prote
24	138	5.5	284	T29001	hypothetical prote
25	122.5	4.9	412	T30079	hypothetical prote
26	122	4.9	1134	T04587	hypothetical prote
27	110	4.4	1234	B36186	I factor protein 2
28	109	4.3	779	JH0102	apolipoprotein B -
29	108	4.3	177	T29000	hypothetical prote

30	105	4.2	733	2	A97415	hypothetical prote
31	104.5	4.2	980	2	H94632	probable receptor-
32	104	4.1	289	2	A38700	cholesteryl ester
33	104	4.1	981	2	T50851	receptor protein k
34	104	4.1	1128	2	A49960	bud emergence prot
35	104	4.1	3005	1	GNVSTV	genome polyprotein
36	103	4.1	693	2	C83821	glycyl-tRNA synthe
37	103	4.1	994	2	H96510	probable disease r
38	102.5	4.1	2218	2	B84683	hypothetical prote
39	101.5	4.0	4924	2	T50176	probable peptide s
40	101	4.0	831	2	H97801	translation initia
41	100.5	4.0	784	2	JH0101	apolipoprotein B-1
42	100	4.0	499	2	E86782	D-alanine activati
43	100	4.0	534	2	G75093	carbamoyl transfer
44	100	4.0	956	2	H81654	conserved hypotnet
45	100	4.0	4307	2	T20721	hypothetical prote

ALIGNMENTS

RESULT 1

A30909

bactericidal/permeability-increasing protein precursor - human

N:Alternate names: SSK bactericidal protein

C:Species: Homo sapiens (man)

C:Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text change 09-Jul-2004

C:Accession: A33850; B54136; A29464; A43600; A49716; A30909

R:Gray, P.W.; Flagg, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.E.; Elsbach, P.

J. Biol. Chem. 264, 9505-9509, 1989

A:Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and

A:Reference number: A33850; MUID:89255455; PMID:2722846

A:Accession: A33850

A:Molecule type: mRNA

A:Residues: 1-487 <GRA>

A:Cross-references: UNIPROT:Q9UCT4; GB:J04739; NID:9179528; PID:AAAS1841.1; PID:gl79529

R:Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.B.; Lane, J.C.; Leon

J. Biol. Chem. 269, 17411-17416, 1994

A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi

A:Reference number: A54136; MUID:94292492; PMID:7517398

A:Accession: B54136

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-374, 'L', 376-487 <WIL>

A:Experimental source: HL-60 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:149855)

R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.

J. Biol. Chem. 262, 14891-14894, 1987

A:Title: A 25-Kda amino-terminal fragment carries all the antibacterial activities of th

A:Reference number: A29464; MUID:88033057; PMID:3667613

A:Accession: A29464

A:Molecule type: protein

A:Residues: 32-51 <OOI>

A:Experimental source: neutrophils

R:Wasiluk, K.R.; Skubitz, K.M.; Gray, B.H.

Infect. Immun. 59, 4193-4200, 1991

A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar

A:Reference number: A43600; MUID:92040097; PMID:1937776

A:Accession: A43600

A:Molecule type: protein

A:Residues: 32-52, 'R' <WAS>

A:Reference number: A49716; MUID:94124531; PMID:8294435

A:Accession: A49716

A:Molecule type: protein

A:Residues: 32-130, 132-141, 143-165, 202-215, 'E', 217-225 <LIT>

C:Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as

which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha

between BPI and an LPS-binding protein from liver and cholesteryl ester transfer protein

C:Genetics:

A:Gene: GDB:BPI

A;Cross-references: GDB:131572; OMIM:109195  
A;Map position: 20q11.23-20q12  
C;Superfamily: lipopolysaccharide-binding protein  
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>  
F;32-51/Region: bactericidal #status predicted  
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 2507; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.4e-186;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRIISQGLDYASQGGTAALQKEL 60  
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRIISQGLDYASQGGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISWPNVGLKFGISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISWPNVGLKFGISNANIKISG 120

Qy 121 KWAQKRFKLMVSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSCSHINSVHVHISKS 180  
Db 121 KWAQKRFKLMVSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKTESALRNKNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKTESALRNKNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSNHNPPPPAPPVMEPPAAHDMVYLGLSDYFPNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGEFYSNHNPPPPAPPVMEPPAAHDMVYLGLSDYFPNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLEL 420  
Db 361 PTGLTFFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLEL 420

Qy 421 HSNIGPFPVELLDQIMNVIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLF 480  
Db 421 HSNIGPFPVELLDQIMNVIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLF 480

Qy 481 GADVYVK 487  
Db 481 GADVYVK 487

RESULT 2  
S10180  
bactericidal permeability-increasing protein precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10180  
R;Leong, S.R.; Camerato, T.  
Nucleic Acids Res. 18, 3052, 1990  
A;Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein  
A;Reference number: S10180; MUID:90272418; PMID:2349103  
A;Accession: S10180  
A;Molecule type: mRNA  
A;Residues: 1-482 <LSO>  
A;Cross-references: UNIPROT:P17453; EMBL:X52563; NID:gl38; PIDN:CAA36797.1; PID:gl39  
C;Superfamily: lipopolysaccharide-binding protein  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>

Query Match 64.9%; Score 1627.5; DB 2; Length 482;  
Best Local Similarity 63.5%; Pred. No. 2.5e-118;  
Matches 306; Conservative 81; Mismatches 94; Indels 1; Gaps 1;

Qy 5 MARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRIISQGLDYASQGGTAALQKELRIK 64

Db 1 MARGPDTARRWATLVVLAALGTAVT-TTNPFGIVARITQKGLDYACQGVLTLLQKLEKIT 59  
Qy 65 IPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISWPNVGLKFGISNANIKISGKWA 124  
Db 60 IPNFSNFKIKYLGKQYFSFVIOGFNLPSQIRPLDKGLDLSIRASIKIRGKWA 119  
Qy 125 OKRFKLMVSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSCSHINSVHVHISKVGW 184  
Db 120 KRNFIKLGNGFDLSVSGISILAGNLGYPASGHSVTTCSSCSGINTVRIHISGSLGW 179  
Qy 185 LIQLFHKKIESALRNKNSQVCEKVTNSVSKLPQYFQTLPVMTKIDSVAGINYLVA 244  
Db 180 LIQLFRKIESLLQKSWTRKICEVTVTSVSSKLPQYFQTLPTVTKLDKAGVDYSLVAPP 239  
Qy 245 ATTAETLDVQMKGEFYSNHNPPPPAPPVMEPPAAHDMVYLGLSDYFPNTAGLVQEA 304  
Db 240 RATANNLDLLKGEFFSLAHRSPPPAPPALAPPDSDRMVYLGISEYFNTAGVYVQA 299  
Qy 305 GVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGL 364  
Db 300 GANLTLRDDMIPEKSKFRLTTKFFGILIPQVAKMFPDMQQLFIWASLPPLTKMFPSSL 359  
Qy 365 TFYPADVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGEKLDRLLELKHNI 424  
Db 360 DLIFVLDTQAFALLPNSSLDPLFLEMLNLSVVVGAKSDRLIGELRLDKLLELKHSDI 419  
Qy 425 GPPVELLDQIMNVIPIVLPRVNEKLOKGFPLTPARVOLNVVLPQHONFLFGADV 484  
Db 420 GPFVESLOSIVNVMPTVLPVINKLOKGFPLPAVIEFNLTLPQYQDFLLFGADV 479  
Qy 485 VY 486  
Db 480 QY 481

RESULT 3  
S43383  
bactericidal/permeability-increasing protein - synthetic  
C;Species: synthetic  
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 20-Oct-1994 #sequence\_revision 15-Feb-1996 #text\_change 15-Feb-1996  
C;Accession: S43383  
R;Qi, S.Y.; Li, Y.; O'Connor, C.D.  
Biochem. J. 238, 711-719, 1994  
A;Title: The region around residue 115 of human bactericidal/permeability-increasing protein of a gene coding for the active domain and characterization of recombinant proteins.  
A;Reference number: S43383  
A;Accession: S43383  
A;Molecule type: DNA  
A;Residues: 1-250 <QIS>

Query Match 51.4%; Score 1288; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 2e-92;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 VNFQVVRISQGLDYASQGGTAALQKELRIKIPDYSDFKIKHLGKGHYFSYMDIRE 91  
Db 2 VNFQVVRISQGLDYASQGGTAALQKELRIKIPDYSDFKIKHLGKGHYFSYMDIRE 61  
Qy 92 FQLPSSQISWPNVGLKFGISNANIKISGKWAQKRFKLMVSGNFDLSIEGMSISADLKL 151  
Db 62 FQLPSSQISWPNVGLKFGISNANIKISGKWAQKRFKLMVSGNFDLSIEGMSISADLKL 121  
Qy 152 SNPTSGKPTITCSSSCSHINSVHVHISKVGWLIQLFHKKIESALRNKNSQVCEKVTN 211  
Db 122 SNPTSGKPTITCSSSCSHINSVHVHISKVGWLIQLFHKKIESALRNKNSQVCEKVTN 181  
Qy 212 SVSKLPQYFQTLPVMTKIDSVAGINYLVAIPATTAETLDVQMKGEFYSNHNPPPP 271  
Db 182 SVSKLPQYFQTLPVMTKIDSVAGINYLVAIPATTAETLDVQMKGEFYSNHNPPPP 241  
Qy 272 PPVMEFPAA 280





Db	67	KIRAVGRQVEPHSLIQSQLRGSSLKPLPGRGLSLISDSSISVRGKWKVRRSPVKLH	126
Qy	133	GNFDLSTEGHSISADLKLGSNPTSGKPTITCCSSCSHINSVHVHISKSKVGLIQLPHKK	192
Db	127	GSFDLDVKSVTISVDLLGVDP--SERPTVTASGCSNRIRDLRHVS--GNVGLNLNLFHNQ	184
Qy	193	IESALRNKMSQVCEKVTNSVSKLOPYFOTLPMTKIDSVAGINYLGLVAPPATTAAETLD	252
Db	185	IESKLOKLVESKICEMIQKSVTSDLOPYLOTLPWTADITILGIDISLVAAPOAKAQTL	244
Qy	253	VOMKGFEYSNNHNPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQAEAGVLKWTLR	312
Db	245	VMEKGEIFNHRSPVTPPTMSLPEDSKQMVYFAISDQAFNIATRVVHQAGYLNFTIT	304
Qy	313	DDMIPKESKRLTTKPGTLPVAKKFPNMKIQIHVSASTPHLSVQPTGLTFYPAVDV	372
Db	305	DDMLPPDSNIRLNKAFRPTPLITRKYPDMNLLELGTVVSAPLLNVSPGNLSLAPQMEI	364
Qy	373	QAFVLPNSSLASFLIGMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGPFPVELL	432
Db	365	EGFVLPSSARESVRLGVVTVNVFVSLTFDNSKVTGMLHPEKAQVRLIESKVGWNVNLF	424
Qy	433	QDIMNYIVPLVPRVNEKLQKGFPLTPARVOLXNVVLQPHQNFLLFGADVYV	486
Db	425	QAFNLVYLLNSLYPDVNDLAKGFPLPRRIKLHDLDFQIHKNFLYLGANVQY	478
RESULT 7			
B35843			
lipopolysaccharide-binding protein - rabbit			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004			
C;Accession: B35843; A46553			
R;Schumann, R.R.; Leong, S.R.; Flaggs, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T			
Science 249, 1429-1431, 1990			
A;Title: Structure and function of lipopolysaccharide binding protein.			
A;Reference number: A35843; MUID:90385281; PMID:2402637			
A;Accession: B35843			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-482 <SCH>			
A;Cross-references: UNIPROT:P17454; GB:M35534; NID:g165467; PIDN:AAA99235.1; PID:g165468			
R;Tobias, P.S.; Soldau, K.; Ulavitch, R.J.			
J. Exp. Med. 164, 777-793, 1985			
A;Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru			
A;Reference number: A46553; MUID:86306528; PMID:2427635			
A;Accession: A46553			
A;Molecule type: protein			
A;Residues: 27-55,'XG','58-62','P',64-65 <TOB>			
C;Superfamily: lipopolysaccharide-binding protein			
C;Keywords: acute phase			
Query Match 39.3%; Score 985.5; DB 2; Length 482;			
Best Local Similarity 40.9%; Pred. No. 1.6e-68;			
Matches 193; Conservative 103; Mismatches 171; Indels 5; Gaps 3;			
Qy	16	VSLMVLVAIGTAVTAANPGVVVIRISQGLDYASQQGTAALQKELKRIKIPDYSDSPKIK	75
Db	14	LSLLIAAAPGALGT---NPGLIITRIDTGLGEYAAAREGLLALQRLLEVTLPDSGDGFRIK	70
Qy	76	HLKGHYSFYSDMIRFQLPSSQI:SMVPNVGLKFSISNANIKSGKWKAKRFLKMSGNF	135
Db	71	HFGRAQYKFSLSKLPREFELLRGTLURPLPGQGLSDISDAIHWKSGWKVRAFLRLKNSP	130
Qy	136	DLSTEGHSISADLKLGSNPTSGKPTITCCSSCSHINSVHVHISKSKVGLIQLPHKKIES	195
Db	131	DLVYKGLTISVHLVLGSE--SSGRPTVITSSCSSDIQNVELDI--EGDLEELNLLQSQIDA	188
Qy	196	ALRNKMSQVCEKVTNSVSKLOPYFOTLPMTKIDSVAGINYLGLVAPPATTAAETLDVQM	255
Db	189	RLRLEVESLTCIQREEAVTAHLQYLOTLPVTTQIDSFAGIDYSLMEAPRATGMLDWMF	248
Qy	256	KGEFYSNNHNPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQAEAGVLKWTLRDDM	315

Db	249	KGEIPDLDRSPVDFLAPAMNLPKASHRMVYFISDYVVENTASLAYHKSGYWNFSITDAM	308
Qy	316	IPKESKRLTTTKFFGCTFLPEVAKKPNMKIQIHVSASTPHLSVQPTGLTFYPAVDVQAF	375
Db	309	VFADLNIRRTTKTSFRPFVPLLANLYPNMNLQGTVTNVSQNLNSTENLEEEPEMDIEAL	368
Qy	376	AVLPNSSLASFLIGHMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGPFPVELLQDI	435
Db	369	VVLPSAREPVRGLGVATNVVSATLINTRKITGFLKPGRLQVELKESKVGGENVELLEAL	428
Qy	436	MNYIVPLVPRVNEKLQKGFPLTPARVOLXNVVLQPHQNFLLFGADVYK	487
Db	429	LNYYILNNLYPKVNEKLAHRFPLEPLRLHTQLYDLDLLQTHENFLLVGANIQYR	480
RESULT 8			
A53533			
phospholipid transfer protein precursor - human			
N;Alternate names: lipid transfer protein II; PLTP			
C;Species: Homo sapiens (man)			
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004			
C;Accession: A53533			
R;Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.L.; Ching, A.F.T.; Grant, F.J.; C			
J. Biol. Chem. 269, 9388-9391, 1994			
A;Title: Complete cDNA encoding human phospholipid transfer protein from human endothelial			
A;Reference number: A53533; MUID:94179366; PMID:8132678			
A;Accession: A53533			
A;Status: preliminary			
A;Molecule type: mRNA			
A;Residues: 1-493 <DAY>			
A;Cross-references: UNIPROT:P50508; GB:L26232; NID:g468325; PIDN:AAA36443.1; PID:g468326			
C;Genetics:			
A;Gene: GDB:PLTP			
A;Cross-references: GDB:340911; OMIM:174245			
A;Map position: 20pter-20qter			
C;Superfamily: lipopolysaccharide-binding protein			
C;Keywords: glycoprotein; phosphoprotein			
F;1-17/Domain: signal sequence #status predicted <SIG>			
F;18-493/Product: phospholipid transfer protein #status experimental <MAT>			
Query Match 18.5%; Score 465; DB 2; Length 493;			
Best Local Similarity 26.9%; Pred. No. 4e-28;			
Matches 124; Conservative 95; Mismatches 214; Indels 28; Gaps 10;			
Qy	34	PGVVVIRISQGLDYASQQGTAALQKELKRIKIPDYSDSPKIKHLGKHG--YSFYSDMIRE	91
Db	20	PGCKIRVTSKALELVKQEGRLPFELETTITPDLRGK-----EGHFYINISEVKVTE	72
Qy	92	FQLPSSQISMVPNVGLKFSISNANIKISGKWKAKRFLKMSGNFDSLIEGMSISADLKL	151
Db	73	LQTSSELDFQFOQELMLQITNASLGLRFRRLLYWFFYDGGYINASAEGVSI RTGLELS	132
Qy	152	SNPTSGKPTITCCSSCSHINSVHVHISKS--KVGWLIQLPHKKIESALRNKMSQVCEKV	209
Db	133	RDP--ACRMKVSNVSCQASVSRMHAFFGGTFKVVYDFLSTP---ITSGMRELLNQIQCPVL	188
Qy	210	TNSVSKLOPYFOTLPMTKIDSVAGINYLGLVAPPATTAAETLDVQMGFEYSNNHN---	266
Db	189	YHAGTVLLNSLLDTVPRSSVDLGVISLMKDPVASTNSLNDMDPFGAFFPITERWNSL	248
Qy	267	PPFPAPVMEFFPAADHDMVYLGLSDYFFNTAGLVQAEAGVLKWTLRDDMIPKESKRLTT	326
Db	249	PNRAVEPQIQ---EERMVYAFSEFFFGSMMESYFRAGALQILLVGDVKVPHDLMLLRA	305
Qy	327	KFFGTFL---PEVAKKFPNMKIQIHVSASTPHLSVQPTGLTFYPAVDVQAFVLPNSSL	383
Db	306	TYFGSIVLLSPAIDS--PLKLERLVA--PPRCTIKPSGTTISVTASVTIALVPPDQPE	361
Qy	384	ASLFLTMHTTGSMEVSAESNRLVGELKDLRLLELKHNSNIGPFPVELLQDIWNYIVPL	443
Db	362	VQLSSMTMDARLSAKMALRGKALRTQLDLRRFRFRIYNNHSALESIALIPLQAPLTKMLQIG	421

```

C;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: AB6141; MUID:21016719; PMID:11130712
A;Accession: C86183
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: UNIPROT:Q9MAU5; GB:AE005172; NID:g7211993; PIDN:AAP40464.1; GSPDB:GN
C;Genetics:
A;Map position: 1

Query Match      13.5%; Score 337.5; DB 2; Length 488;
Best Local Similarity 23.6%; Pred. No. 3.1e-18;
Matches 109; Conservative 87; Mismatches 240; Indels 25; Gaps 11;

Qy    38 VRISQGLDYASQQCTAAQLKELRKIKIPDYSDFPKI KHLGKHGYFSYMDIREFQLPSS 97
Db    31 VLVSQGDLFDVKNLLVNKAIAIIPIQIPRIEKSMKIPFLGGIDVVVSNLTIVELDVA 90
Qy    98 QISMVPNVNGLKFSINANIKISKRWKAQRK-----LKMNGNFILSIEGMSISADLKLG 151
Db    91 YVKL-GETGVVIVAAGTTCNLNMWHYSYSTWLPPIEISDOGIASVQVCMEIG--LSLG 147
Qy    152 SNPTSGKPTITCCSCSHINSVHVHISKVGWLIOLFHKKIESALRNKNNSQVCEKVTN 211
Db    148 LKSDDEGLKLSLSECGCHEVDITI EL-EGGAWFYQGMVNAFKDQIGSSVESTIAKLTE 206
Qy    212 SVSSKLPQPYFTPLPWTKIDSVAGNYGLVAPATTAEITLDVMOKGEFY--SENHNPPPP 269
Db    207 GVSD-LDSFLOSLKPEIPDDNADLNVTTSDPILNRSSTIFFEIDLGTGETNQVLKSF 265
Qy    270 PAPPV-MEFPAADRMYLVGLSDYFPNTAGLVYQEAGVLKMTLRDDMPKESKRLTTKF 328
Db    266 FKKSLSVLICPGNSKMLGISVDEAVFNSEAALYNADFQWVV--DKIPQS--LLNTAR 321
Qy    329 FGTLPPEVAKFPNNMKIQIHVSASTPPHLSVQPTGLTFTPADVQA---FAVLPNSSLAS 385
Db    322 WRFIIPQLYKKYPNDMMNLNISLSPPLVKISEQ----YGVANNADLVINVLDANQVIP 377
Qy    386 LFLGMHTTGSMWEASERNLVELKLDRLLLEKHSNIIGPPVPELLQDIMNYIVPIVL 445
Db    378 VACISLMTRGSALRMVGNLGLSVLEDFSMCLKWSNIGNLHLHLLOPIVWTVIQTVFV 437
Qy    446 PRVNEKLGQGPPLPPARPVLNVVVLQPQNELLFGADVY 486
Db    438 PYANDHLEKGFLPIMHGFTLQNAEICSESEITVCSDVAY 478

RESULT 11
A26941
cholesterol ester transfer protein precursor - human
C;Species: Homo sapiens [man]
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A26941
R;Drayna, D.; Jarnagin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lawn, R.
Nature 327, 632-634, 1987
A;Title: Cloning and sequencing of human cholesterol ester transfer protein cDNA.
A;Reference number: A26941; MUID:87258172; PMID:3600759
A;Accession: A26941
A;Molecule type: mRNA
A;Residues: 1-493 <DRA>
A;Cross-references: UNIPROT:P11597; EMBL:M30185; NID:g180259; PIDN:AAA51977.1; PID:g1802
C;Genetics:
A;Gene: GDB:CETP
A;Cross-references: GDB:1119773; OMIM:118470
A;Map position: lqlq13-16ql3
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-493/Product: cholesterol ester transfer protein #status predicted <MAT>

```

Query Match 11.8%; Score 295; DB 2; Length 493;  
Best Local Similarity 23.7%; Pred. No. 6.2e-15;  
Matches 116; Conservative 92; Mismatches 243; Indels 38; Gaps 16;

QY 17 SLMLVAIGPAVTAAV-----NPGVVVRIISQKGLDYASQQGTAALQKELKRIKIPDYSDF 72  
DB 5 TVTLLALLGNAHACSGKTSHEAGIVCRITKPALLVLNHETAKVIQTAFQASVPDITGEK 64  
QY 73 KIKHLKGHYSPYSDIMREIFQLPSSQISMPVNVGLKFSISNANIKISGKWK---AQKRF 129  
DB 65 AMMLLGQVYKGLHNIQISHLSIASQSVELVEAKSIDVSIGNVSVVFKGLKYGYTTAWML 124  
QY 130 KMSGNFDLSIEGHSISADLKLGNPT--SGKPTITCSSCSSHINSVHVHI--SKSKVGM 186  
DB 125 GIDQSIDFEIDS---AIDLQINTQLTCDSGRVRTDAPDCVLSFHKLLHLQGEREPGWI 181  
QY 187 QLPHKKTIESALRNKNMSQVEKVTNSVSSKLOQYFOTLPVMTKIDSVAGINYGLVAPPAT 246  
DB 182 QLFTNFISFTLKLVLKQICKET--NVISNIMADPVQTRAASILSDGIDGVIDLSLTGDPVI 240  
QY 247 TASTLDVQMKGEYSENHNHP---PPFAPVPMFEPPAAHDMVMVYGLSDYFFNTAGLVYOE 303  
DB 241 TASYLESHHKGHYFTIKYXVSBDLPLPTFSPDLL---GDSRMLYFWFSERVFHSLAKVAF 296  
QY 304 AGVLKMTLRDMDIPKESKFLTTTKFCT---FLPEYAKKPPNMKIOIHVSASTPHLSVQ 360  
DB 297 DGRMLUSLMGD---EPKAVLETWGFNTNQEIFQEVVGGFPS--QAQTVHCLKMPKISQ 351  
QY 361 PTGLTFYPADVQAFVALPNS--SLASFLIGHMHTGSMSEVSAESNRLVGELKDLRLLE 418  
DB 352 NKGWVNVSSVMVFLPRPDQOHSVAVTFEEDIVTT--VQASYSKKKLLFSL--LDFOITP 408  
QY 419 LKHSNTGPPFVELLODMVIVILVILPRVNEKLOKGF-PLTPPARVOLYNNV---LQPH 474  
DB 409 KTVSNLTESSESIQFLOSMITAVGIPEVMSRLEVVFYFTALMNSKGVSLFDIINPIIR 468  
QY 475 QNFLFLFGAD 483  
DB 469 DGFLLQMD 477

RESULT 12  
A53176  
C:Species: Macaca fascicularis (crab-eating macaque)  
C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C:Accession: A53176  
R:Pape, M.E.; Renberg, E.F.; Marotti, K.R.; Melchior, G.W.  
Arterioscler. Thromb. 11, 1759-1771, 1991  
A:Title: Molecular cloning, sequence, and expression of cynomolgus monkey cholesterol  
asma high density lipoprotein levels.  
A:Reference number: A53176; MUID:92031355; PMID:1931878  
A:Accession: A53176  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-493 <PAP>  
A:Cross-references: GB:M86343

Query Match 11.2%; Score 282; DB 2; Length 493;  
Best Local Similarity 23.8%; Pred. No. 6.4e-14;  
Matches 111; Conservative 89; Mismatches 233; Indels 34; Gaps 15;

QY 35 GVVVRIISQKGLDYASQQGTAALQKELKRIKIPDYSDFKIKHLKGHYSPYSDIMREFQL 94  
DB 27 GIVCRITKPALLVLNQETAKVIQSAQFQANVPNITGEKAMMLLGQVYKGLHNIQISHLSI 86  
QY 95 PSSQISMPVNVGLKFSISNANIKISGKWK---AQKRELKMSGNFDLSIEGHSISADLKL 151  
DB 87 ASRRLVELVEAKSIDVSIGNVSVVFKGLKYGYTTAWGLIGIDQSDVDFEIDS---AIDLQIN 143  
QY 152 SNPT--SGKPTITCSSCSSHINSVHVHI--SKSKVGM 208  
DB 144 TVTCDGSRVBTAPDCVLSFHKLLHLQGEREPGWIQTFTNFI SPTIKLVLKGOICKE 203

Db 401 SANLSVALRTEAKAVSNLTESRSESQSSLRSLATVGIPEWGRLEVAFTALNMNSKGLD 460  
Qy 466 LYNVV 470  
Db 461 LFEII 465

RESULT 14  
S17447  
probable ligand-binding protein RY2G5 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 22-May-1998 #text\_change 05-Nov-1999  
C:Accession: S17447  
R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.  
EMBO J. 10, 2813-2819, 1991  
A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfactory  
A:Reference number: S17447; MUID:92007724; PMID:1915264  
A:Accession: S17447  
A:Molecule type: mRNA  
A:Residues: 1-470 <DEA>  
A:Cross-references: EMBL:X60660; NID:g57731; PIDN:CAA43067.1; PID:g57732  
A:Experimental source: olfactory mucosa  
C:Genetics:  
A:Gene: RY2G5  
C:Keywords: olfaction

Query Match 10.4%; Score 261.5; DB 2; Length 470;  
Best Local Similarity 22.4%; Pred. No. 2.3e-12; Mismatches 20; Indels 27; Gaps 11;  
Matches 90; Conservative 80

Qy 89 IREFOLPSSQISMVNVGLKFSISNANIKISKGKWAQKRFKMGNFDSIEGMSISADL 148  
Db 84 IVELTLPRVSVRLPGVGYLSL-YTRVAINGK-----SLIGFLDIAVE-VNITAKV 133

Qy 149 KLGSNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLFHKKIESALRNKMSQVCEK 208  
Db 134 RLTMRT-GYPLRVIERCDTLGGIKVKLLR---GLLPNLVNLVNRVLNVLPLDLC-P 188

Qy 209 VTNSSVSKLQPYFQTLPVMTKIDSVAGINYLVAAPPATTAEITLDVQMK-----GEFVS 261  
Db 189 IVDVVLGLVNDQLGVDSLVPIGLIGSVQYTFSSPLVTGFELELDLNLVGEAGDLD 248

Qy 262 ENHNHPPFPAPPVM-EFFAAHDM-VYLGSLDYFFNTAGLVYQEAQVLMKTLRDDMIPKE 319  
Db 249 YLGRPAMLPRQMPLELPPMGDNTNSQLAISANFLSVLTMQLKQGLDIDITDGMF--E 306

Qy 320 SKFRLTTFEFTFLPEVAKKFNMK-IQIHVSASTPPHLSVQPTGLTFYPADVQVAFVL 378  
Db 307 DLPLTTSTLGLALPKVFOQYPSRPLTIRIQVNPPTVTLOKRALVKVFATSEVVVSQ 366

Qy 379 PNSSLASFLIGHHTTGSMEVSAENRVLGELKLDRLLELKHNSIGPPVELLODIMNY 438  
Db 367 PNDVETICLDVDVLDLASFVEGKLMIDAKLDKTSNLNRTSNVGNFDFILEMLVEK 426

Qy 439 IVPILVLRVNEKLOKGFPLTPARVQLNVNVVLQPHQNFLL 479  
Db 427 IFDLAFMPANNAILGSGVPLKILNIDFSNADIVLEDLLV 467

RESULT 15  
S17448  
probable ligand-binding protein RYA3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S17448  
R:Dear, T.N.; Boehm, T.; Keverne, E.B.; Rabbitts, T.H.  
EMBO J. 10, 2813-2819, 1991  
A:Title: Novel genes for potential ligand-binding proteins in subregions of the olfactory  
A:Reference number: S17447; MUID:92007724; PMID:1915264  
A:Accession: S17448  
A:Status: preliminary  
A:Molecule type: mRNA

A:Residues: 1-473 <DEA>  
A:Cross-references: EMBL:X60658; NID:g57733; PIDN:CAA43065.1; PID:g57734

Query Match 9.4%; Score 234.5; DB 2; Length 473;  
Best Local Similarity 21.8%; Pred. No. 2.9e-10;  
Matches 109; Conservative 88; Mismatches 229; Indels 75; Gaps 18;

Qy 13 PRVSLMVLVAIGTAVTAANVP-GVVVRISQKGLDYASQ---GTAALQKELKRIK---- 64  
Db 3 PGVYALLMLGLATPCGLLETVGTARIDKDELGAQNSLVGGPILQNVLTGTVTSVQ 62

Qy 65 -----IPDYSDSPKIKHLGKHGHSFYFMDIREFQLPSSQISMVNVGLKFSI 111  
Db 63 GLLGAGLLGGGSLSGFLSVEELSG-----LKIEELTLFVSKILPGVGVQVLSL 116

Qy 112 SNANIKISGKWAQKRFKMGNFDSIEGMSISADLKLGSNPTSGKPTITCSSSSHIN 171  
Db 117 -HTKVSLLHSGS-----PLVGLLQAAE-VNVSSKVALGMSP-RGTPIILKRC---N 162

Qy 172 SVHVHISKSKVGLIQLFHKKIESALRNKMSQVCEKVTNSVSSKQLQPYFQTLPVMTKID 231  
Db 163 TLLGHISLTS-GLLPTPIFGLVEQTLCKVLPGLLC-PVVDVSVLVSVNELLGATLSLPLG 220

Qy 232 SVAGINYLVAAPPATTAEITLDVQMKGEFYSNHNHP--PPAPPVMEFPAA----- 280  
Db 221 PLGSVEFTLATPLISNQYIELDI-----NPIVKSIAQDVDPKPRLPVMPPK 270

Qy 281 --HDMVYVLGLSDYFFNTAGLVYQEAQVLMKTLRDDMIPKSKFLRTTKFTFLPEVAK 338  
Db 271 EDHTSQVTVPL--YLFNTVFGLLQTNGALDLDITPEMYP--NIFLTITDLAALAPEALG 326

Qy 339 KPP---NMKIQIHVSASTPPHLSVQPTGLTFYPADVQVAFVLNSSLASFLIGHHTTG 395  
Db 327 KLPPCQHLLLSLRVMSK--PMILLQNKVTVSIPVTIHLSSVPOQTPTVALFQMGVMTL 384

Qy 396 SMEVSAENRVLGELKLDRLLELKHNSIGPPVELLODIMNYIVPILVLRVNEKLOKQ 455  
Db 385 NAHLVPSTTKLHISLSLERLTQVLASSPQSFDAERLEEWLSDVVVRAAYMQLNEHLEVG 444

Qy 456 FPLTPARVQLNVNVVLQPHQN 476  
Db 445 IPLPKILNVNFAVSVDVVIEN 465

Search completed: October 21, 2005, 11:31:47  
Job time : 41.7407 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 64.7154 Seconds  
(without alignments)  
1455.954 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193

Perfect score: 943

Sequence: 1 CNAPRWVSLMVLVAIGTAVT.....HVHISKSKVGLVQLFHKKI 184

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	943	100.0	483	1	BPI_HUMAN	P17213 homo sapien
2	939	99.6	487	2	Q81W58	Q81W58 homo sapien
3	688	73.0	179	2	Q9GK39	Q9GK39 macaca mula
4	596.5	63.3	482	1	BPI_BOVIN	P17453 bos taurus
5	567.5	60.2	482	2	Q6AXU0	Q6AXU0 rattus norv
6	554.5	58.8	483	2	Q67E05	Q67E05 mus musculus
7	554.5	58.8	486	2	Q8BSF3	Q8BSF3 mus musculus
8	518.5	55.0	178	2	Q9GK40	Q9GK40 oryctolagus
9	506.5	53.7	445	1	BPI_RABIT	Q28739 oryctolagus
10	448	47.5	481	1	LBP_MOUSE	Q61805 mus musculus
11	429	45.5	477	2	Q8TCF0	Q8TCF0 homo sapien
12	429	45.5	481	1	LBP_HUMAN	P18428 homo sapien
13	428	45.4	481	1	LBP_RAT	Q63313 rattus norv
14	394	41.8	476	2	Q6GLX0	Q6GLX0 xenopus lae
15	357.5	37.9	482	1	LBP_RABIT	P17454 oryctolagus
16	312.5	33.1	473	2	Q773Q8	Q773Q8 gadus morhu
17	312.5	33.1	473	2	Q773Q9	Q773Q9 gadus morhu
18	312.5	33.1	473	2	Q804Q9	Q804Q9 cyprinus ca
19	312	33.1	473	2	Q8JFX3	Q8JFX3 oncorhynch
20	311.5	33.0	473	2	Q8JFX4	Q8JFX4 oncorhynch
21	222.5	23.6	477	2	Q81W29	Q81W29 crassostrea
22	197.5	20.9	507	1	BPI2_HUMAN	Q8N1Q6 homo sapien
23	186.5	19.8	509	1	BPI2_MOUSE	Q8C186 mus musculus
24	172.5	18.3	493	1	PLTP_MOUSE	P55065 mus musculus
25	169	17.9	493	1	PLTP_HUMAN	P55058 homo sapien
26	166	17.6	496	2	Q8WMN7	Q8WMN7 sus scrofa
27	156	16.5	48	2	Q864W2	Q864W2 sus scrofa
28	153.5	16.3	503	2	Q8WNG5	Q8WNG5 oryctolagus
29	153.5	16.3	503	2	Q95JG0	Q95JG0 oryctolagus
30	148	15.7	483	2	Q66IU4	Q66IU4 xenopus lae
31	141	15.0	486	2	Q6DEI0	Q6DEI0 brachydanio

RESULT 1

ID	BPI_HUMAN	STANDARD	PRT	483 AA
AC	P17213, Q9BY29; Q9H1L2; Q9H1M8; Q9H203; Q9UD65;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Bactericidal permeability-increasing protein precursor (BPI) (CAP 57).			
GN	Name=BPI;			
OS	Homo sapiens (Human);			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.			
RX	MEDLINE=89255455; PubMed=2722846;			
RA	Gray P.W., Flagg G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,			
RA	Elsbach P.;			
RT	"Cloning of the cDNA of a human neutrophil bactericidal protein.			
RT	Structural and functional correlations.";			
RL	J. Biol. Chem. 264:9505-9509(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94292492; PubMed=7517398;			
RA	Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,			
RA	Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;			
RT	"Bactericidal/permeability-increasing protein and lipopolysaccharide			
RT	(LPS)-binding protein. LPS binding properties and effects on LPS-			
RT	mediated cell activation.";			
RL	J. Biol. Chem. 269:4741-47416(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT ALA-12.			
RA	Xu J., Wang H.;			
RT	"Cloning of cDNA of human bactericidal/permeability-increasing			
RT	protein.";			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANTS ALA-12 AND GLU-212.			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaeslaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,			

32	139.5	14.8	485	2	Q9BG59	Q9BG59 tupaia gliis
33	130.5	13.8	493	1	CETP_HUMAN	P11597 homo sapien
34	129.5	13.7	489	1	YSV5_CABEL	Q10011 caenorhabdi
35	129.5	13.7	497	1	CETP_RABIT	P22687 oryctolagus
36	120.5	12.8	493	1	CETP_MACFA	P47896 macaca fasc
37	113.5	12.0	515	2	Q8VYC2	Q8VYC2 arabidopsis
38	112	11.9	42	2	Q9N0U2	Q9N0U2 sus scrofa
39	110	11.7	551	2	Q93796	Q93796 caenorhabdi
40	110	11.7	573	2	Q6RV01	Q6RV01 caenorhabdi
41	105	11.1	22	2	Q9UCT4	Q9UCT4 homo sapien
42	103	10.9	458	1	BPI_L_HUMAN	Q8N4F0 homo sapien
43	103	10.9	458	2	Q6UMN3	Q6UMN3 homo sapien
44	103	10.9	458	2	Q6ZME0	Q6ZME0 homo sapien
45	102	10.8	606	2	Q18869	Q18869 caenorhabdi

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Rangeay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Shra H.K., Shownkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.,  
RA "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
RN [5]  
RN SEQUENCE OF 28-42.  
RP MEDLINE=88033057; PubMed=3667613;  
RX Ooi C.E., Weiss J., Elsbach P., Frangione B., Mannion B.;  
RA "A 25-kDa NH2-terminal fragment carries all the antibacterial  
RT activities of the human neutrophil 60-kDa bactericidal/permeability-  
RT increasing protein.";  
RL J. Biol. Chem. 262:14891-14894(1987).  
RN [6]  
RN SEQUENCE OF 28-47.  
RX MEDLINE=89315847; PubMed=2501794;  
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,  
RA Marra M.N., Seeger M., Nathan C.F.;  
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=97334442; PubMed=9189532; DOI=10.1126/science.276.5320.1861;  
RA Beamer L.J., Carroll S.F., Eisenberg D.;  
RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A  
RT resolution.";  
RL Science 276:1861-1864(1997).  
CC -1- FUNCTION: The cytotoxic action of BPI is limited to many species  
CC of Gram-negative bacteria; this specificity may be explained by a  
CC strong affinity of the very basic N-terminal half for the  
CC negatively charged lipopolysaccharides that are unique to the  
CC Gram-negative bacterial outer envelope.  
CC -1- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
CC leukocytes (PMN) granules.  
CC -1- TISSUE SPECIFICITY: Restricted to cells of the myeloid series.  
CC -1- DOMAIN: The N-terminal region may be exposed to the interior of  
CC the granule, whereas the C-terminal portion may be embedded in the  
CC membrane. During phagocytosis and degranulation, proteases may be  
CC released and activated and cleave BPI at the junction of the N-  
CC and C-terminal portions of the molecule, providing controlled  
CC release of the N-terminal antibacterial fragment when bacteria are  
CC ingested.  
CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: J04739; AAA51841.1; ALT INIT.  
CC EMBL: AF322588; AAG42844.1; -.  
CC EMBL: AL359555; CAC13043.1; -.  
CC EMBL: AL499625; CAC27350.1; -.  
CC EMBL: AL391692; CAC10453.1; -.  
CC EMBL: P0B; 1BP1; X-ray; @=28-483.  
CC EMBL: P0B; 1EWF; X-ray; @=28-483.  
CC EMBL: HGNC:1095; BPI.  
CC MIM: 109195; -.  
CC GO: GO:0005887; C: integral to plasma membrane; TAS.  
CC InterPro: IPR001124; LBP\_BPI\_CETP.  
CC Pfam: PF01273; LBP\_BPI\_CETP; 1.  
CC Pfam: PF02886; LBP\_BPI\_CETP\_C; 1.

DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BPI2; 1.  
DR PROSITE: PS00400; LBP\_BPI\_CETP; 1.  
KW 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;  
KW Polymorphism; Signal; Transmembrane.  
FT SIGNAL 1 27  
FT CHAIN 28 483 Bactericidal permeability-increasing  
FT protein.  
FT SITE 236 241 Cleavage sites for elastase (Potential).  
FT TRANSMEM 365 385 Potential.  
FT VARIANT 12 12 V -> A (in dbSNP:1341023).  
FT VARIANT 192 192 A -> V (in dbSNP:5743509).  
FT VARIANT 212 212 /FTId=VAR\_018402.  
FT VARIANT 212 212 K -> E (in dbSNP:4358188).  
FT CONFLICT 351 351 /FTId=VAR\_018403.  
FT CONFLICT 371 371 P -> S (in Ref. 3).  
FT CONFLICT 400 400 F -> L (in Ref. 2).  
FT CONFLICT 407 407 N -> D (in Ref. 3).  
FT CONFLICT 407 407 K -> R (in Ref. 3).  
FT STRAND 32 37  
FT HELIX 38 56  
FT TURN 57 58  
FT STRAND 64 67  
FT STRAND 77 89  
FT STRAND 93 98  
FT TURN 99 101  
FT STRAND 102 122  
FT TURN 123 124  
FT STRAND 125 149  
FT TURN 150 153  
FT STRAND 154 165  
FT STRAND 168 172  
FT HELIX 176 178  
FT HELIX 179 188  
FT TURN 189 189  
FT HELIX 190 211  
FT TURN 212 212  
FT HELIX 213 217  
FT TURN 218 219  
FT STRAND 223 225  
FT STRAND 231 233  
FT STRAND 236 236  
FT STRAND 241 242  
FT STRAND 246 251  
FT STRAND 254 256  
FT STRAND 281 286  
FT HELIX 287 299  
FT TURN 300 301  
FT STRAND 304 308  
FT HELIX 309 311  
FT TURN 314 315  
FT STRAND 321 321  
FT HELIX 322 326  
FT TURN 327 328  
FT HELIX 332 335  
FT TURN 337 338  
FT STRAND 340 346  
FT STRAND 352 356  
FT TURN 357 358  
FT STRAND 359 363  
FT STRAND 365 373  
FT TURN 375 376  
FT STRAND 379 388  
FT STRAND 391 397  
FT STRAND 401 408  
FT STRAND 412 418  
FT HELIX 425 428  
FT HELIX 429 439  
FT TURN 440 440  
FT HELIX 441 450  
FT STRAND 452 453  
FT TURN 458 459



```
FT STRAND 460 470
FT TURN 471 472

Query Match 100.0%; Score 943; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.7e-75; Indels 0; Gaps 0;
Matches 184; Conservative 0; Mismatches 0;

Qy 1 CNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
Db 6 CNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65
Qy 61 DSFKIKHLGKHGHSFYFSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120
Db 66 DSFKIKHLGKHGHSFYFSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 125
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVWLIQLF 180
Db 126 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVWLIQLF 185
Qy 181 HKKI 184
Db 186 HKKI 189

RESULT 2
Q8IW58 PRELIMINARY; PRT; 487 AA.
AC Q8IW58;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein..
GN Name=BPI;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish U., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC040955; AAH40955.1; -.
DR HSSP; P17213; 1EWF.
DR GO; GO:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
```

```
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
SQ SEQUENCE 487 AA; 53880 MW; FE709D9317E5206D CRC64;

Query Match 99.6%; Score 939; DB 2; Length 487;
Best Local Similarity 99.5%; Pred. No. 8.4e-75; Indels 0; Gaps 0;
Matches 183; Conservative 0; Mismatches 1;

Qy 1 CNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
Db 10 CNAPRWYSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 69
Qy 61 DSFKIKHLGKHGHSFYFSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120
Db 70 DSFKIKHLGKHGHSFYFSDMIREFOLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 129
Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVWLIQLF 180
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHSHSKVGVWLIQLF 189
Qy 181 HKKI 184
Db 190 HKKI 193

RESULT 3
Q9GK39 PRELIMINARY; PRT; 179 AA.
AC Q9GK39;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein (fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu J., Wang H.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF322587; AAG42843.1; -.
DR HSSP; P17213; 1EWF.
DR GO; GO:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; SM00328; BPI1; 1.
FT NON TER 1
FT NON TER 179 179
SQ SEQUENCE 179 AA; 19772 MW; F1B180A02A38CE63 CRC64;

Query Match 73.0%; Score 688; DB 2; Length 179;
Best Local Similarity 88.2%; Pred. No. 5.1e-53; Indels 0; Gaps 0;
Matches 134; Conservative 9; Mismatches 9;

Qy 33 QKGLDYASQOQTAALQKELKRIKIPDYSDFSPKIKHLGKHGHSFYFSDMIREFOLPSSQISM 92
Db 1 QKGLDYASQOQTAALQKELKRIKIPDYSDFSPKIKHLGKHGHSFYFSDMIREFOLPSSQISM 60
Qy 93 VPNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
Db 61 VPNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 120
Qy 153 TCSCSSHNSVHVHSHSKVGVWLIQLFHKKI 184
Db 121 SCSCSSHNSVHVHSHSKVGVWLIQLFHKKI 152

RESULT 4
BPI_BOVIN
ID BPI_BOVIN
AC P17453; PRT; 482 AA.
```

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bactericidal permeability-increasing protein precursor (BPI).  
 GN Name=BPI;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RX MEDLINE=90272418; PubMed=2349103;  
 RA "Leong S.R., Camerato F.;  
 RT Nucleotide sequence of the bovine bactericidal permeability  
 RL Nucleic Acids Res. 18:3052-3052(1990).  
 CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
 CC of Gram-negative bacteria; this specificity may be explained by a  
 CC strong affinity of the very basic N-terminal half for the  
 CC negatively charged lipopolysaccharides that are unique to the  
 CC Gram-negative bacterial outer envelope.  
 CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
 CC Leukocytes (PMN) granules (By similarity).  
 CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
 CC similarity).  
 CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
 CC the granule, whereas the C-terminal portion may be embedded in the  
 CC membrane. During phagocytosis and degranulation, proteases may be  
 CC released and activated and cleave BPI at the junction of the N-  
 CC and C-terminal portions of the molecule, providing controlled  
 CC release of the N-terminal antibacterial fragment when bacteria are  
 CC ingested (By similarity).  
 CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/announcements>/  
 CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
 CC -----  
 DR EMBL; X52563; CAA36797.1; -;  
 DR PIR; S10180; S10180.  
 DR HSP; P17213; LEWF.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
 DR Antibiatic; Glycoprotein; Membrane; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 482 Bactericidal permeability-increasing  
 FT protein.  
 FT SITE 235 240  
 FT CARBOHYD 62 62 Cleavage sites for elastase (Potential).  
 FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 389 389 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 482 AA; 53432 MW; DD7D5AE785BC42D CRC64;  
 Query Match 63.3%; Score 596.5; DB 1; Length 482;  
 Best Local Similarity 63.2%; Pred. No. 2e-44;  
 Matches 115; Conservative 29; Mismatches 37; Indels 1; Gaps 1;  
 QY 3 APRVSLMLVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPYSDS 62  
 DB 8 ARRWATLVLAALGTAVT-TTNPQIVARITQKGLDYACQOQGLTLQKLEKITIPNPSGN 66

QY 63 FKIKHLGKHGYSFYSDIREFOLPSSQISMPVNPVGLKFSISNANIKISGKWKAKRFLKM 122  
 DB 67 FKIKLGRKQYFFSFWISQIRPLNPSQIRPLDKGLDLSIRDASIKIRGKWKAKRQFIKL 126  
 QY 123 SGNFDLSIEGMSISADLKLGNSPTSGKPTTICSSSCSHINSVHVHSKSVGWLIOLFHK 182  
 DB 127 GGNFDLSVSGISILAGNLGYDPASGHSVTTCSSCSGGINTVRIHISGSLGLWLIQLFK 186  
 QY 183 KI 184  
 DB 187 RI 188  
 RESULT 5  
 Q6AXUO PRELIMINARY; PRT; 482 AA.  
 ID Q6AXUO  
 AC Q6AXUO;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Bactericidal/permeability-increasing protein.  
 GN Name=Bpi;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,  
 RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences.";  
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Director MGC Project;  
 RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; BC079318; AAH79318.1; -;  
 DR GO; GO:0008289; Filipid binding; IEA.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP\_1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 SQ SEQUENCE 482 AA; 53751 MW; 269591C4C2F5A6D1 CRC64;

Query Match 60.2%; Score 567.5; DB 2; Length 482;  
 Best Local Similarity 59.6%; Pred. No. 7.6e-42;  
 Matches 109; Conservative 29; Mismatches 44; Indels 1; Gaps 1;  
 QY 2 NAFVSLMLVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPYSD 61  
 DB 7 NVKWSLLALTAIVGTALTAATDPGFVARISQKGLDFVCOESMVLEQKELLAISIPFSG 66

```
QY 62 SFKIKHLGKHGHSFYSDMIREQLPSSQISWPNVGLKFSISNANIKISGKWKAQKRLK 121
Db 67 DFKIKHLGKGTVEFYSDMAVEGPHIDPQIKLLPSDGLQLSITSASIKISGRWYKRNILK 126
QY 122 MSGNFDLSTEGMSISADLKLGNPTSGKPTTICSSCSHNSVHVHISKSKVGLWLIQLPH 181
Db 127 ASGNFQLSIQGVSIITADILGNPD-SGRITITCTCDSHNSVRIKSGSMLGWLILQLPH 185
QY 182 KKI 184
Db 186 RKI 188
RESULT 6
Q67E05 PRELIMINARY; PRT; 483 AA.
AC Q67E05;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Bactericidal/permeability-increasing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Bingle C.D., Craven J.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY363993; AAR13289.1; -.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 483 AA; 53940 MW; 4AA24D8095C52B74 CRC64;
Query Match 58.8%; Score 554.5; DB 2; Length 483;
Best Local Similarity 57.9%; Pred. No. 1.1e-40;
Matches 106; Conservative 33; Mismatches 43; Indels 1; Gaps 1;
QY 2 NAPRVSLMLVLAIGTAVTAANVGVVRSIQGLDYASQQGTAALQKELKIKIPDYSD 61
Db 7 NVKWSALLLAIIGTALTAATDPGRVAMISQGLDFACQGVWELQKELQALISVPDFSG 66
QY 62 SFKIKHLGKHGHSFYSDMIREQLPSSQISWPNVGLKFSISNANIKISGKWKAQKRLK 121
Db 67 VFKIKHLGKGSYEFYSMAVDGFHINPKIEMLPDGLRVFIKDSIKINGRWMSRKNFLK 126
QY 122 MSGNFDLSTEGMSISADLKLGNPTSGKPTTICSSCSHNSVHVHISKSKVGLWLIQLPH 181
Db 127 AGNFPQLSIQGVSIITADILGSD-SSGHITTCNSCDSHDSVHVHISGMLGWLIRLPH 185
QY 182 KKI 184
Db 186 RKI 188
RESULT 7
Q8BSF3 PRELIMINARY; PRT; 486 AA.
AC Q8BSF3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mus musculus adult male epididymis cDNA, RIKEN full-length enriched
DE library, clone 9230105K17 product: weakly similar to
DE bactericidal/permeability-increasing protein.
GN Name=9230105K17Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
```

```
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN PANTOM Consortium;
RL "Functional annotation of a full-length mouse cDNA collection.";
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RA The PANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RL "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RL "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RL "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Epididymis;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura K.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK033770; BAC28468.1; -.
DR HSSP; P17213; 1BP1.
DR MGD; GGI:3045315; 9230105K17Rik.
DR CO; GO:0008289; F.lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 486 AA; 54351 MW; 9D8F627EA5496D62 CRC64;
```

Query Match

58.8%; Score 554.5; DB 2; Length 486;

```
Best Local Similarity 57.9%; Pred. No. 1.le-40;
Matches 106; Conservative 33; Mismatches 43; Indels 1; Gaps 1;

QY 2 NAPRWLMVLVAIGTAVTAANPVGVRVRSQKGLDYASQOGTAALQKELKRIKIPDYS 61
Db 7 NVKWSALLLAIGTALTATDPGFVAMISQKGLDFACQGVVLEQKELQALISVDFSG 66
QY 62 SFKIKHLGKHGHSFYSDIRFQPSQISQWPNVGLKFSISNANIKISGKWAQKFLX 121
Db 67 VFKIKHLGKGSYFYSNAVDGPHIPNKIEMLPDGLRVFIKDAKINGKWSRKNFLK 126
QY 122 MSGNFDLSIGMSTADLKLGSNPTSGKPRITSCSSSHNSVHVHISKSKVGWLIQLFH 181
Db 127 AGNFELISIQGVISTDLILGSD-SSGHITTCNSCDSHDSVHIKISGMLGWLRLFH 185
QY 182 KKI 184
Db 186 RKI 188

RESULT 8
Q9GK40 PRELIMINARY; PRT; 178 AA.
AC Q9GK40;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Bactericidal/permeability-increasing protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RA Xu J., Wang H.;
RP SUBMITTED (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF322586; AAG42842.1; -.
DR HSP; P17213; 1BP1.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR SMART; SM00328; BPI1; 1.
FT NON_TER 1 178
FT NON_TER 178 178
SQ SEQUENCE 178 AA; 19693 MW; 867D7C6CA14B3A75 CRC64;

Query Match 55.0%; Score 518.5; DB 2; Length 178;
Best Local Similarity 62.5%; Pred. No. 5.5e-38;
Matches 95; Conservative 29; Mismatches 27; Indels 1; Gaps 1;

QY 33 QKGLDYASQOGTAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDIRFQLPSSQISM 92
Db 1 QKGLDYACQGVAVLQKELKIRIPDVSGFKLPFPFGKGHYNFHSVLRVSRFQLPNPQIRL 60
QY 93 VPNVGLKFSISNANIKISGKWAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
Db 61 QPNVGLRVISNANVRIGRWKARKGFIKVRGKFDLSVEGVSISADLKLGSPASGRATV 120
QY 153 TCSSCSHNSVHVHISKSKVGWLIQLFHKKI 184
Db 121 TCSSCSNINRRLRVSGILGWLKLFHKRI 151

RESULT 9
BPI_RABIT STANDARD; PRT; 445 AA.
AC Q28739;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bactericidal permeability-increasing protein (BPI) (Fragment).
GN Name=BPI;
OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RA Weiss J., Weinrauch Y., Levy O., Flynn S.;
RP SUBMITTED (JUN-1996) to the EMBL/GenBank/DBJ databases.
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The cytotoxic action of BPI is limited to many species of gram-negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the gram-negative bacterial outer envelope (By similarity).
CC -!- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear leukocytes (PMN) granules (By similarity).
CC -!- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By similarity).
CC -!- DOMAIN: The N-terminal region may be exposed to the interior of the granule, whereas the C-terminal portion may be embedded in the membrane. During phagocytosis and degranulation, proteases may be released and activated and cleave BPI at the junction of the N- and C-terminal portions of the molecule, providing controlled release of the N-terminal antibacterial fragment when bacteria are ingested (By similarity).
CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP family.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
-----
EMBL; U61270; AAB03812.1; -.
DR HSP; P17213; 1BP1.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00328; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; PARTIAL.
KW Antibiotic; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 1 1
FT SITE 198 203 Cleavage sites for elastase (Potential).
FT TRANSMEM 327 347 Potential.
FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 445 AA; 48837 MW; 209AE0894FEDACFC CRC64;

Query Match 53.7%; Score 506.5; DB 1; Length 445;
Best Local Similarity 62.5%; Pred. No. 1.8e-36;
Matches 95; Conservative 26; Mismatches 30; Indels 1; Gaps 1;

QY 33 QKGLDYASQOGTAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDIRFQLPSSQISM 92
Db 1 QKGLDYACQGVAVLQKELKIRIPDVSGFKLPFPFGKGHYNFHSVLRVSRFQLPNPQIRL 60
QY 93 VPNVGLKFSISNANIKISGKWAQKRLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTI 152
Db 61 QPNVGLRVISNANVRIGRWKARKGFIKVRGKFDLSVEGVSISADLKLGSPASGRATV 120
QY 153 TCSSCSHNSVHVHISKSKVGWLIQLFHKKI 184
Db 121 TCSSCSNINRRLRVSGILGWLKLFHKRI 151

RESULT 10
LBP_MOUSE
ID LBP_MOUSE STANDARD; PRT; 481 AA.
AC Q61805; Q99XA0;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)  
Lipopolysaccharide-binding protein precursor (LBP).  
Name=Lbp;  
Mus musculus (Mouse).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
NCBI\_TaxID=10090;  
(1)  
SEQUENCE FROM N.A.  
STRAIN=BALB/c;  
MEDLINE=97289150; PubMed=9144073;  
Lengacher S., Jongeneel C.V., le Roy D., Lee J.D., Kravchenko V.,  
Ulevitch R.J., Glauser M.P., Heumann D.;  
"Reactivity of murine and human recombinant LPS-binding protein (LBP)  
within LPS and Gram-negative bacteria";  
J. Inflamm. 47:165-172(1995).  
(2)  
SEQUENCE FROM N.A.  
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Richards S., Worley K.C., Hale S.A., Malek J.A., Gunaratne P.H.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting J.M., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
-!- FUNCTION: Binds to the lipid moiety of bacterial  
lipopolysaccharides (LPS), a glycolipid present in the outer  
membrane of all Gram-negative bacteria. The LBP/LPS complex seems  
to interact with the CD14 receptor.  
-!- SUBCELLULAR LOCATION: Secreted.  
-!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
family.  
-----  
This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
EMBL; X99347; CAA67727.1; -;  
DR EMBL; BC004795; AAH04795.1; -;  
DR HSP; P12133; LEWP  
DR MGD; MG1:1098776; Lbp.  
DR GO; GO:0001530; F:lipopolysaccharide binding; IDA.  
DR InterPro; IPR001124; LBP\_BPI\_CETP.  
DR Pfam; PF01273; LBP\_BPI\_CETP; 1.  
DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BPI2; 1.  
DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
KW Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.  
FT SIGNAL 1 24 Potential.  
FT CHAIN 25 481 Lipopolysaccharide-binding protein.  
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).  
FT CONFLICT 25 25 C -> G (in Ref. 2).  
FT CONFLICT 51 51 K -> Q (in Ref. 2).  
FT

FT CONFLICT 102 102 R -> S (in Ref. 2).  
FT CONFLICT 280 280 A -> S (in Ref. 2).  
FT CONFLICT 310 310 H -> P (in Ref. 2).  
FT CONFLICT 313 313 G -> S (in Ref. 2).  
FT CONFLICT 341 341 R -> G (in Ref. 2).  
FT CONFLICT 382 382 S -> G (in Ref. 2).  
FT CONFLICT 395 396 TR -> NS (in Ref. 2).  
FT CONFLICT 418 418 I -> M (in Ref. 2).  
SQ SEQUENCE 481 AA; 53312 MW; 34EA9C066C9AB678 CRC64;  
  
Query Match 47.5%; Score 448; DB 1; Length 481;  
Best Local Similarity 47.0%; Pred. No. 3e-31;  
Matches 85; Conservative 43; Mismatches 51; Indels 2; Gaps 2;  
  
Qy 4 PRWVSLMVLVAIGPVTAAVNPVGVVRSIQKGLDYASQOQTAALQKELKRIKIPIDYSDSP 63  
Db 7 PLLSTLGLLFLSLIQGTGCVNPGVARITDKGLAYAAKEGLVALKRELYKITLPDFSGDF 66  
  
Qy 64 KIKHLGKHGHSFYSDMIREFQLPSSQISMPVNVGLKFSISNANIKISGKWKAKQKFLKMS 123  
Db 67 KIKAVGRGOYEFHSLQNCLELRSGLSLKLPQOQLRLAISDSSIGVRGKWKVRKSLFLKLH 126  
  
Qy 124 GNFDLSLEGMSISADLKLGNPTSGKPTITCSCSSSHNSVHVHISKSKVGLIQLPHKK 183  
Db 127 GSFLLDVRGVITISVDLLLGMDP-SGRPTVSASGSSRICDLDVHIS-GNVGLNLNLFHQ 184  
  
Qy 184 I 184  
Db 185 I 185  
  
RESULT 11  
Q8TCF0 PRELIMINARY; PRT; 477 AA.  
ID Q8TCF0  
AC Q8TCF0;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE LBP protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Richards S., Worley K.C., Hale S.A., Malek J.A., Gunaratne P.H.,  
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting J.M., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Strausberg R.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022256; AAH22256.1; -.









Qy 7 VSLMVLVAIGTAVTAANPGVVRISOKGLDYASOQGTAAQKELKRIKIPDYSDFKIK 66  
Db 14 LSLLLAAAPGALGT---NPLITRITDKGLEYAAREGLLALQKLEVTLPDSGDGDFRIK 70  
Qy 67 HLGKGHYSFYSDIREFOLPSSQISMVNVGLKFSISNANIKISGKWKAKRFLKMSGNF 126  
Db 71 HFGRQYKPYSLKIPRFELLRGTLRPLPQOGLSLDISDAYIHVRGSWKVRKAPLELKNPF 130  
Qy 127 DLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKSKVGMWLIQLFHKKI 184  
Db 131 DLYVKGLTISVHLVLGSE-SSGRPTVTTSKSSDIONVELDI-EGDLELLNLLQSQI 186

Search completed: October 21, 2005, 11:30:50  
Job time : 66.7154 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 171.285 Seconds  
(without alignments)  
1455.954 Million cell updates/sec

Title: US-10-629-516-2  
Perfect score: 2507  
Sequence: 1 MRENARGPCNAPRWVSLMV.....NVQLQHQNFLFGADVVK 487

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2500	99.7	487	2	Q81W58
2	2486	99.2	483	1	BPI HUMAN
3	1627.5	64.9	482	1	BPI BOVIN
4	1507.5	60.1	445	1	BPI RABIT
5	1415.5	56.5	482	2	Q6AXU0
6	1361	54.3	483	2	Q67E05
7	1349.5	53.8	486	2	Q8BSF3
8	1145.5	45.7	476	2	Q6GLX0
9	1088	43.4	481	1	LBP HUMAN
10	1062	42.4	477	2	Q8TGF0
11	1039	41.4	481	1	LBP RAT
12	1030	41.1	481	1	LBP MOUSE
13	985.5	39.3	482	1	LBP RABIT
14	870.5	34.7	473	2	Q8JFX3
15	867.5	34.6	473	2	Q8JFX4
16	867	34.6	473	2	Q804Q9
17	814	32.5	473	2	Q7T3Q8
18	814	32.5	473	2	Q7T3Q9
19	811	32.3	179	2	Q9GK39
20	621.5	24.8	178	2	Q9GK40
21	541	21.6	507	1	BPL2 HUMAN
22	500.5	20.0	509	1	BPL2_MOUSE
23	465	18.5	493	1	PLTP_HUMAN
24	463.5	18.5	493	1	PLTP_MOUSE
25	452.5	18.0	477	2	Q817Z9
26	450	17.9	496	2	Q8WMN7
27	434	17.3	483	2	Q661U4
28	433.5	17.3	503	2	Q8WNQ5
29	433.5	17.3	503	2	Q95UG0
30	425	17.0	486	2	Q6DE10
31	386.5	15.4	515	2	Q8VYC2

Query Match 99.7% Score 2500 DB 2 Length 487

32	337.5	13.5	488	2	Q9MAU5
33	336.5	13.4	488	2	Q8LAL8
34	317	12.6	1424	2	Q9LTR5
35	295	11.8	493	1	CETP_HUMAN
36	287	11.4	458	2	Q6UWN3
37	283	11.3	458	2	Q6ZME0
38	282	11.2	127	2	Q9NOL9
39	282	11.2	493	1	CETP_MACFA
40	278	11.1	458	1	BPI_HUMAN
41	271.5	10.8	497	1	CETP_RABIT
42	267.5	10.7	485	2	Q9BG59
43	261.5	10.4	470	1	LPC4_RAT
44	260.5	10.4	462	1	BPI_MOUSE
45	252.5	10.1	449	1	BPL3_MOUSE

## ALIGNMENTS

RESULT 1  
Q81W58 PRELIMINARY; PRT; 487 AA.  
AC Q81W58;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Bactericidal/permeability-increasing protein.,  
GN Name=BPI;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX STRAUSBERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
MEDLINE=223888257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX STRAUSBERG R.;  
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
EMBL; BC040955; AAH40955.1; -.  
DR HSP; PI7213; 1EWP.  
DR GO; GO:0008289; F.lipid binding; IEA.  
DR InterPro; IPR001124; LBP\_BPI\_CETP.  
DR Pfam; PF01273; LBP\_BPI\_CETP; 1.  
DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
DR SMART; SM00328; BPI1; 1.  
DR SMART; SM00329; BPI2; 1.  
DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
SQ SEQUENCE 487 AA; 53860 MW; FE709D9311E5206D CRC64;

```
Best Local Similarity 99.6%; Pred. No. 2.2e-181;
Matches 485; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWISLMLVLAIGTAVTAANPGVVVRISQKGLDVASQOQGTAAALQKEL 60
Db 1 MRENLRGPCNAPRWISLMLVLAIGTAVTAANPGVVVRISQKGLDVASQOQGTAAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKHGHSYPSMDIREFQLPSSQISWPNVNGVKFISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKHGHSYPSMDIREFQLPSSQISWPNVNGVKFISNANIKISG 120

Qy 121 KWKAQKFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKS 180
Db 121 KWKAQKFLKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHNSVHVHISKS 180

Qy 181 KVGWLIQLFHKHTESALRNKNSQVCEKVTNSVSSKLQYFQTLPVMTKIDSIVAGINYL 240
Db 181 KVGWLIQLFHKHTESALRNKNSQVCEKVTNSVSSKLQYFQTLPVMTKIDSIVAGINYL 240

Qy 241 VAPPATTAETLDVOMKGEFYSENNHNPFPAPPVMEFPAAHDMVYLGSLDYFENTAGLV 300
Db 241 VAPPATTAETLDVOMKGEFYSENNHNPFPAPPVMEFPAAHDMVYLGSLDYFENTAGLV 300

Qy 301 YQEAGVLKMTLRDDIMPKESKFRLLTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDIMPKESKFRLLTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLRLLLELK 420
Db 361 PTGLTFFPAVDVQAFVLPNSSLASLFLIGHHTTGSMEVSAESNRLVGLKLRLLLELK 420

Qy 421 HSNIGPFPVELLDIMNIVPILVPRVNEKLGKGFPLTPARVOLNVVQLPHQNFLLF 480
Db 421 HSNIGPFPVELLDIMNIVPILVPRVNEKLGKGFPLTPARVOLNVVQLPHQNFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 2
BPI_HUMAN
ID_BPI_HUMAN STANDARD; PRT: 483 AA.
AC P17213; Q9BYZ9; Q9HL12; Q9H1M8; Q9H203; Q9UD65;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Bactericidal permeability-increasing protein precursor (BPI) (CAP 57).
GN Name=BPI;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-64.
RX MEDLINE=99255455; PubMed=2722846;
RA Gray P.W., Flagg G., Leong S.R., Gumina R.J., Weiss J., Ooi C.E.,
RA Eisbach P.;
RT "Cloning of the cDNA of a human neutrophil bactericidal protein.
RT Structural and functional correlations.";
RL J. Biol. Chem. 264:9505-9509(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292492; PubMed=7517398;
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT (LPS)-binding protein. LPS binding properties and effects on LPS-
RT mediated cell activation.";
RL J. Biol. Chem. 269:17411-17416(1994).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ALA-12.
RA Xu J., Wang H.;
```

```
RT "Cloning of cDNA of human bactericidal/permeability-increasing
RT protein.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS ALA-12 AND GLU-212.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Scavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hutt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehaealaho M.H., Leveraha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.B., McConnachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showken R., Sims S.,
RA Stuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whithead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE OF 28-42.
RX MEDLINE=88033057; PubMed=3667613;
RA Ooi C.E., Weiss J., Elebach P., Frangione B., Mannion B.;
RT "A 25-kDa NH2-terminal fragment carries all the antibacterial
RT activities of the human neutrophil 60-kDa bactericidal/permeability-
RT increasing protein.";
RL J. Biol. Chem. 262:14891-14894(1987).
RN [6]
RP SEQUENCE OF 28-47.
RX MEDLINE=89315847; PubMed=2501794;
RA Gabay J.E., Scott R.W., Campanelli D., Griffith J., Wilde C.,
RA Marra M.N., Seeger M., Nathan C.F.;
RT "Antibiotic proteins of human polymorphonuclear leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:5610-5614(1989).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97334442; PubMed=9189532; DOI=10.1126/science.276.5320.1861;
RA Beamer L.J., Carroll S.F., Eisenberg D.;
RT "Crystal structure of human BPI and two bound phospholipids at 2.4-A
RT resolution.";
RL Science 276:1861-1864(1997).
RN [8]
RP -I- FUNCTION: The cytotoxic action of BPI is limited to many species
RP of Gram-negative bacteria; this specificity may be explained by a
RP strong affinity of the very basic N-terminal half for the
RP negatively charged lipopolysaccharides that are unique to the
RP Gram-negative bacterial outer envelope.
RP -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear
RP Leukocytes (PMN) granules.
RP -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series.
RP -I- DOMAIN: The N-terminal region may be exposed to the interior of
RP the granule, whereas the C-terminal portion may be embedded in the
RP membrane. During phagocytosis and degranulation, proteases may be
RP released and activated and cleave BPI at the junction of the N-
RP and C-terminal portions of the molecule, providing controlled
RP release of the N-terminal antibacterial fragment when bacteria are
RP ingested.
RP -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
RP family.
RN [9]
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

```

-----
CC EMBL; J04739; AAA51841.1; ALT INIT.
CC EMBL; AF322588; AAG42844.1; -
CC EMBL; AL359555; CAC13043.1; -
CC EMBL; AL459625; CAC27350.1; -
CC EMBL; AL391692; CAC10453.1; -
CC PDB; 1BPI; X-ray; @=28-483.
CC PDB; 1EWF; X-ray; A=28-483.
CC Genew; HGNC:1095; BPI.
CC MIM; 109195; -
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC InterPro; IPR001124; LBP_BPI_CETP.
CC Pfam; PF01273; LBP_BPI_CETP; 1.
CC Pfam; PF02886; LBP_BPI_CETP_C; 1.
CC SMART; SM00328; BPI1; 1.
CC SMART; SM00329; BPI2; 1.
CC PROSITE; PS00400; LBP_BPI_CETP; 1.
KW 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;
KW Polymorphism; Signal; Transmembrane.
FT SIGNAL 1 27
FT CHAIN 28 483 Bactericidal permeability-increasing
FT SITE 236 241 Protein.
FT TRANSMEM 365 385 Cleavage sites for elastase (Potential).
FT VARIANT 12 12 Potential.
FT VARIANT 192 192 V -> A (in dbSNP:1341023).
FT VARIANT 212 212 A -> V (in dbSNP:5743509).
FT VARIANT 351 351 K -> E (in dbSNP:4358188).
FT CONFLICT 371 371 P -> S (in Ref. 3).
FT CONFLICT 400 400 F -> L (in Ref. 2).
FT CONFLICT 407 407 N -> D (in Ref. 3).
FT STRAND 32 37 K -> R (in Ref. 3).
FT HELIX 38 56
FT TURN 57 58
FT STRAND 64 67
FT STRAND 77 89
FT STRAND 93 98
FT TURN 99 101
FT STRAND 102 122
FT TURN 123 124
FT STRAND 125 149
FT TURN 150 153
FT STRAND 154 165
FT STRAND 168 172
FT HELIX 176 178
FT STRAND 179 188
FT TURN 189 189
FT HELIX 190 211
FT TURN 212 212
FT STRAND 213 217
FT TURN 218 219
FT STRAND 223 225
FT STRAND 231 233
FT STRAND 236 236
FT STRAND 241 242
FT STRAND 246 251
FT STRAND 254 256
FT STRAND 281 286
FT HELIX 287 299
FT TURN 300 301
FT STRAND 304 308
FT HELIX 309 311
FT TURN 314 315

```

```

FT STRAND 321 321
FT HELIX 322 326
FT TURN 327 328
FT HELIX 332 335
FT TURN 337 338
FT STRAND 340 346
FT STRAND 352 356
FT TURN 357 358
FT STRAND 359 363
FT STRAND 365 373
FT TURN 375 376
FT STRAND 379 388
FT STRAND 391 397
FT STRAND 401 408
FT STRAND 412 418
FT HELIX 425 428
FT HELIX 429 439
FT TURN 440 440
FT HELIX 441 450
FT STRAND 452 453
FT TURN 458 459
FT STRAND 460 470
FT TURN 471 472

Query Match 99.2%; Score 2486; DB 1; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-180;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MARGPCNAPRWSLMVLVAIGTAVTAANPVGVVVRISQKGLDYASQQGTAALQKELKRIK 64
DB 1 MARGPCNAPRWSLMVLVAIGTAVTAANPVGVVVRISQKGLDYASQQGTAALQKELKRIK 60
QY 65 IPDYSDFSFKIKHLGKGYHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWK 124
DB 61 IPDYSDFSFKIKHLGKGYHYSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWK 120
QY 125 QKRFKMSGNPDLISIEGMSISADLKGSNPTSGKPTITCSCSCSHINSVHVHISKSKYGM 184
DB 121 QKRFKMSGNPDLISIEGMSISADLKGSNPTSGKPTITCSCSCSHINSVHVHISKSKYGM 180
QY 185 LIQLFHKKIESALRNKNMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYLGLVAPP 244
DB 181 LIQLFHKKIESALRNKNMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYLGLVAPP 240
QY 245 ATTAETLDVQMGGEFYSENHNHPPFPAPPVMEFPAADHDMVYLGISDYFFNTAGLVQEA 304
DB 241 ATTAETLDVQMGGEFYSENHNHPPFPAPPVMEFPAADHDMVYLGISDYFFNTAGLVQEA 300
QY 305 GVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNMKIQIHVSASTPHLSVQPTGL 364
DB 301 GVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFPNNMKIQIHVSASTPHLSVQPTGL 360
QY 365 TFYPADVQVQAFVLPNSSLSLFLIGHMTTCSMEVSASNRIVGELKLDRLLELKHSNI 424
DB 361 TFYPADVQVQAFVLPNSSLSLFLIGHMTTCSMEVSASNRIVGELKLDRLLELKHSNI 420
QY 425 GPPFVELLDIMNYIVPILVPRVNEKIQKGFPLPTPARVOLYNNVLPQHNFLFGADV 484
DB 421 GPPFVELLDIMNYIVPILVPRVNEKIQKGFPLPTPARVOLYNNVLPQHNFLFGADV 480
QY 485 VYK 487
DB 481 VYK 483

RESULT 3
BPI_BOVIN
ID BPI_BOVIN STANDARD; PRT; 482 AA.
AC P17453;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bactericidal permeability-increasing protein precursor (BPI).

```

GN Name=BPI;  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Bone marrow;  
 RA MEDLINE=90272418; PubMed=2349103;  
 RX Leong S.R., Camerato T.;  
 RT "Nucleotide sequence of the bovine bactericidal permeability  
 RL Nucleic Acids Res. 18:3052-3052(1990).  
 CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
 CC of Gram-negative bacteria; this specificity may be explained by a  
 CC strong affinity of the very basic N-terminal half for the  
 CC negatively charged lipopolysaccharides that are unique to the  
 CC Gram-negative bacterial outer envelope.  
 CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
 CC Leukocytes (PMN) granules (By similarity).  
 CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
 CC similarity).  
 CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
 CC the granule, whereas the C-terminal portion may be embedded in the  
 CC membrane. During phagocytosis and degranulation, proteases may be  
 CC released and activated and cleave BPI at the junction of the N-  
 CC and C-terminal portions of the molecule, providing controlled  
 CC release of the N-terminal antibacterial fragment when bacteria are  
 CC ingested (By similarity).  
 CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; X52563; CAA36797.1; -.  
 DR PIR; S10180; S10180.  
 DR HSP; P17213; IEF.  
 DR InterPro; IPR001124; LBP\_BPI\_CETP.  
 DR Pfam; PF01273; LBP\_BPI\_CETP; 1.  
 DR Pfam; PF02886; LBP\_BPI\_CETP\_C; 1.  
 DR SMART; SM00328; BPI1; 1.  
 DR SMART; SM00329; BPI2; 1.  
 DR PROSITE; PS00400; LBP\_BPI\_CETP; 1.  
 KW Antibiotic; Glycoprotein; Membrane; Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 482  
 FT  
 FT SITE 235 240 Bactericidal permeability-increasing  
 FT Cleavage sites for elastase (Potential).  
 FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 375 375 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 389 389 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 482 AA; 53432 MW; DD7D59AE785BC42D CRC64;  
 Query Match 64.9%; Score 1627.5; DB 1; Length 482;  
 Best Local Similarity 63.5%; Pred. No. 4.4e-115;  
 Matches 306; Conservative 81; Mismatches 94; Indels 1; Gaps 1;  
 QY 5 MARGPCNAPWVSIWLVLTGTAATVAVNPGVVRISQKGLDYASQGTAAOLKELKRIK 64  
 DB 1 MARGPDPTARWATLVLAALGTAVT-TTNPGIVARITQKGLDYACQGVLTLOKLEKIT 59  
 QY 65 IPDYSDFKIKHLGKHGHSYFSYMDIREFQLPSSQISMPVNVGKFSISNARIKISGWKA 124  
 DB 60 IPNFGNFKIKYLGKGYSFFSMVIOGNLPNSQIRPLPKGLDLSIRDASIKIRGWKA 119

QY 125 QKFLKMSGNFDLSLEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKVKVG 184  
 DB 120 RKNFIKLGNGFDLSVEGISILAGNLGYDPASGHSTVTCSSSGSINTVRIHISGSLGW 179  
 QY 185 LIQLFHKKIESALRNKQNSQVCEKVTNSVSSKLQPYFQTLPMVMTKIDSVAGINYLVA 244  
 DB 180 LIQLFRKRIESLLQKSMTRKICEVTVSTVSSKLQPYFQTLPTVTKLDKAGVDVSLV 239  
 QY 245 ATTAETLDVOMKGEFYSNHNHPPPPAPVPMVEFFPAAHDMVYLGLSDYFPNTAGLV 304  
 DB 240 RATANLNDLLKGEFFSLAHRSPPPAPPALAPPSSDHRMVLGISEYFFENTAGFY 299  
 QY 305 GVLKMTLRDMDPKESKFLTKFFGTFPLPEVAKKPNMKIQIHVSASTPHLSVOP 364  
 DB 300 GALLNLTFRDMDPKESKFLTKFFGILIPQVAKMFPDMQMFIVASLPPKLTMKPSS 359  
 QY 365 TFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKH 424  
 DB 360 DLIFVLDTQAFALLPNSSLDPLLEMLNLSVVGAKSDRLIGELRLDKLLELKH 419  
 QY 425 GPPFVELLDQIMNYIVPILVLRVNEKLOKGPPLPTPARVOLVNVVLQPHONELL 484  
 DB 420 GPFVESLQSVINYVMTIVLPVINKLKQKGFPLPLPAYIEFLNLTLPQYQDFLE 479  
 QY 485 VY 486  
 DB 480 QY 481  
 RESULT 4  
 BPI\_RABIT STANDARD; PRT; 445 AA.  
 ID BPI\_RABIT  
 AC Q28739;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bactericidal permeability-increasing protein (BPI) (Fragment).  
 GN Name=BPI;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=New Zealand white; TISSUE=Bone marrow;  
 RA Weiss J., Weinrauch Y., Levy O., Flynn S.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -I- FUNCTION: The cytotoxic action of BPI is limited to many species  
 CC of Gram-negative bacteria; this specificity may be explained by a  
 CC strong affinity of the very basic N-terminal half for the  
 CC negatively charged lipopolysaccharides that are unique to the  
 CC Gram-negative bacterial outer envelope (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Membrane-associated in polymorphonuclear  
 CC Leukocytes (PMN) granules (By similarity).  
 CC -I- TISSUE SPECIFICITY: Restricted to cells of the myeloid series (By  
 CC similarity).  
 CC -I- DOMAIN: The N-terminal region may be exposed to the interior of  
 CC the granule, whereas the C-terminal portion may be embedded in the  
 CC membrane. During phagocytosis and degranulation, proteases may be  
 CC released and activated and cleave BPI at the junction of the N-  
 CC and C-terminal portions of the molecule, providing controlled  
 CC release of the N-terminal antibacterial fragment when bacteria are  
 CC ingested (By similarity).  
 CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP  
 CC family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

```
CC -----
CC EMBL: U61270; AAB03812.1; -.
CC HSSP: P17213; LBPI.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP; 1.
DR Pfam: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
DR PROSITE: PS00400; LBP_BPI_CETP; PARTIAL.
KW Antibiotic; Glycoprotein; Transmembrane.
FT NON_TER 1
FT SITE 198 203 Cleavage sites for elastase (Potential).
FT TRANSMEM 327 347 Potential.
FT CARBOHYD 352 352 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 445 AA; 48837 MW; 209AE0894FEDACFC CRC64;
```

```
Query Match 60.1%; Score 1507.5; DB 1; Length 445;
Best Local Similarity 63.0%; Pred. No. 5.2e-106;
Matches 279; Conservative 80; Mismatches 83; Indels 1; Gaps 1;

QY 42 QKGLDYASQGTAAQKELKRIKIPDYSDFKIKHLGKGHYSFYSDIREFOLPSSQISM 101
DB 1 QKGLDYACQGVAVLQKELEKIRIPDVSGFKLRPFKGYHNFHSLVRSFOLPNPQIRL 60

QY 102 VNVGLKFSISNANIKISKWKAQKRFKMGNFOLSIIEGMSISADLKLGSNPTSGKPTI 161
DB 61 QNVGLRVISNANVRIGRWKARKGFIKVRGKFDLSVEGVSISADLKLGSVPASGRATV 120

QY 162 TCSSCSSHNSVHVHISKVWGLIQLFHKKIESALRNQNSQVCEKVTNSVSSKLQPYF 221
DB 121 TCSSCSSHNSNRRARLSQASGCGWL-KLFHKRIESSLRNTMNSKIQCVLTSSVSKLQPVV 179

QY 222 QTLPMWTKIDSAGINYGAVAPATTAETLDVQMGGEFYSNNHNPFPFAPVMEFPAAH 281
DB 180 ETPLPKERLDSVAGIDYLSVAPPRATADSLDQMGGEFYNNVAPRPPPPMPMAIPSLH 239

QY 282 DRMWYGLSDYFNTAGLVYQAGVLMKTRDMDMPKESKFRITTKFFGTFTLPEVAKFP 341
DB 240 DRMWYLAISDYLFNTAALVYQAGAGFLTRDMDMPKESKRLTKFLGKALPQVAKMFP 299

QY 342 NMKIQIHVSASTPPHLSVQPTGLTFYPADVQAFVLPNSLSIASLFLIGHMTTGSMEVSA 401
DB 300 NMNVQLTSSVSPPHLTTRPTGIALTAADVQLQAFALPNSLSIASLFLGLKLNTSAKIGT 359

QY 402 ESNRLVGLKLRLLLELKHNSIGPPVELLDINNYVPIVLPRVNEKLQKGFPLTP 461
DB 360 KADKLVGELTLGRLLLELKHNSIGSPFVQLQALMDYVLSAVVLPKVNKELQKGFPLPMP 419

QY 462 ARVOLNVVLQPHONFLFGADV 484
DB 420 RKVQLYDLVLQPHQDFLLGNV 442
```

```
RESULT 5
Q6AXU0 PRELIMINARY; PRT; 482 AA.
ID Q6AXU0 AC Q6AXU0
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Bactericidal/permeability-increasing protein.
GN Name=Bpi.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
```

```
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Caeavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBSJ databases.
EMBL: BC079318; AAH79318.1; -.
DR GO: GO:0008289; F:lipid binding; IEA.
DR InterPro: IPR001124; LBP_BPI_CETP.
DR Pfam: PF01273; LBP_BPI_CETP; 1.
DR Pfam: PF02886; LBP_BPI_CETP_C; 1.
DR SMART: SM00328; BPI1; 1.
DR SMART: SM00329; BPI2; 1.
SQ SEQUENCE 482 AA; 53751 MW; 269591C42CF5A6D1 CRC64;
```

```
Query Match 56.5%; Score 1415.5; DB 2; Length 482;
Best Local Similarity 55.8%; Pred. No. 5.7e-99;
Matches 268; Conservative 89; Mismatches 122; Indels 1; Gaps 1;

QY 5 MARGPCNAPRWVSLMVLVAIGTAVTAANNPVGWVVRISOKGLDYASQGTAAQKELKRIK 64
DB 1 MAWGPDNVRKWSLLALLAIVGTALTAAATDPGFVARISOKGLDFVQCESMVELQKELLALS 60

QY 65 IDPYSDSFKIKHLGKGHYSFYSDIREFOLPSSQISMPNVGLKFSISNANIKISKWKA 124
DB 61 IDPDSGDKIRHLGKGTYEFYSMAVEGHIPDPQIKLPSDGLQLSITSASIKISRWKY 120

QY 125 QKRFLKMGNFOLSIIEGMSISADLKLGSNPTSGKPTITCSSCSSHNSVHVHISKVGM 184
DB 121 RKNILKASGNFOLSIQGVSLIADLILGNPD-SGRITITCSTCDSHNSVRIKVSGLMW 179

QY 185 LIQLFHKKIESALRNQNSQVCEKVTNSVSSKLQPYFQTLPMVKIDSVAGINYLGVAPP 244
DB 180 LIQLFHRKIETSLKTIYKICKIVRNSVSAKLQPYVKTLPVAVKVDITSDISLLAPP 239

QY 245 ATTAETLDVQMGGEFYSNNHNPFPFAPVMEFPAADHBMVYGLSDYFNTAGLVYQEA 304
DB 240 MTTDKFLEGQLRGEPFWRGHGHPFAPVPMVNNILPNNNYMVCMSIDYFNTAEPAQES 299

QY 305 GVLKMTLRDMDIPKESKFRITTKFFGTFTLPEVAKFPNNMKIQIHVSASTPPHLSVQPTGL 364
DB 300 ETLKITLRDQLLAKADARYHLNTDFLTKTFLPEVAKFPNSMGLQLLISAPLFAHLNIQPSGL 359

QY 365 TFYPADVQAFVLPNSLSIASLFLIGHMTTGSMEVSAESNRLVGEKLRLLLELKHNSI 424
DB 360 SILSPNLETRAFVVLFPNSSLIPLFLGKMTNASLEVNAMKNRLIGEMKLRLLLELQKSNF 419

QY 425 GPFVELLDINNYVPIVLPRVNEKLQKGFPLTPPARVOLNVVLQPHONFLFGADV 484
DB 420 GSKFVELLEDVINYLMSTWVLPKINEKLRGRGFPPLPPLPAGIQLNLSILYSQNFLLLEADL 479
```

```
RESULT 6
Q67E05 PRELIMINARY; PRT; 483 AA.
ID Q67E05
AC Q67E05;
```





```
SQ SEQUENCE 486 AA; 54351 MW; 908F627EA5496D62 CRC64;
Query Match 53.8%; Score 1349.5; DB 2; Length 486;
Best Local Similarity 53.7%; Pred. No. 6e-94;
Matches 260; Conservative 90; Mismatches 129; Indels 5; Gaps 3;
QY 5 MARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQGLDYASQOQTAAALQKELKRIK 64
DB 1 MTWAPDNVRKWSALLLAIIGTALTAAATDPGFVAMISQGLDFACQOQGWELQELQAIS 60
QY 65 IPDYSDSFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKESISNANIKISGKWKA 124
DB 61 VPDESGVFVKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKESISNANIKISGKWKA 120
QY 125 QKRFLKMGNFPLDSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKSKVGW 184
DB 121 RKNFLKAGNFELSIOGVSISTDLILGSD-SSGHITTCNSCHSDSHDSVHIKISGMLGW 179
QY 185 LIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFOTLPVMTKIDSVAGINYLVAAPP 244
DB 180 LIRLFPHRKIETSLKNIYKICKIVRDSVSKLOPYLTKLSTVITRVDDVTSDVSYLLAPL 239
QY 245 ATTAETLDVOMKEGFYSNHNPPPPFAPVMEFFPAAHDMVYVGLSDYFENTAGLVQEA 304
DB 240 TTTNQFLEGQLGGEFFWGRHDPDLPPIHPPVVRFPVNGAYMCMGSDYFENTVLAQQS 299
QY 305 GVLKMTLRDDMIKPKESKFLRTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQPTGL 364
DB 300 GTLKMTLGQLLSNNGRQLNTDFLRTFLPKVAKNFPMSGVQLLISAPVPHLSIQPSGL 359
QY 365 TTFYPAVDVQAFVLPNSLASLFLIGM--HTTGSMEVSAESNRNLVGBELK-DRLLLELK 420
DB 360 SFNPKLETQAFVLPNASLVPFLVGMVRRKTNASLEVDABENRVLGEMKLSRWLELK 419
QY 421 HSNITGPPVELLDQIMNVIPLVLPVRYNEKLOKGFPLTPARVOLYNNVLOPHONFLIF 480
DB 420 ESKGFPFVXELEDVINYLVSTLVLPKINERLRGFPFLPLPAGIRFSHTFTFYFYNQFLL 479
QY 481 GADV 484
DB 480 EADL 483
```

## RESULT 8

```
O6GLX0 PRELIMINARY; PRT; 476 AA.
ID O6GLX0
AC O6GLX0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE MGC84153 protein.
GN Name=MGC84153;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
```

```
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klein S., Gehard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074326; AAH74326.1;
DR GO; GO:0008289; P:lipid binding; IEA.
DR InterPro; IPR005503; FILL.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF03748; FIL1; 1.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
SQ SEQUENCE 476 AA; 52117 MW; 595F36DB5AB8B05D CRC64;
Query Match 45.7%; Score 1145.5; DB 2; Length 476;
Best Local Similarity 45.7%; Pred. No. 1.9e-78;
Matches 221; Conservative 99; Mismatches 155; Indels 9; Gaps 3;
QY 4 NMARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQGLDYASQOQTAAALQKELKRI 63
DB 2 NIAYG-----LTFLSMAAPVGTATDGTGNGFVVRLTKGLDYALQEGMIVLQQLPQI 54
QY 64 KIPDYSDFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKESISNANIKISGKW 123
DB 55 QLPDPSGTGYDVGVLGKVKYRFSSMTISSVQLPSYQVIVPDKGLKLSISGAFIQVDGRWD 114
QY 124 AQKRFKMGNFPLDSIEGMSISADLKLSNPTSGKPTITCSCSSHINSVHVHISKSKVG 183
DB 115 VRYSEFIHEDGSFNKVLGISISVGLIGSD-ESGRPTIAPSDCSCHISNVEVHMS-GTIG 172
QY 184 WLIIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFOTLPVMTKIDSVAGINYLVA 243
DB 173 WLVDLFHNNVESLRSQSMENKICPEVTQSISSKLLPLLQTLPTVTKIDQISAIQSLTGP 232
QY 244 PATTAETLDVOMKEGFYSNHNPPPPFAPVMEFFPAAHDMVYVGLSDYFENTAGLVQ 303
DB 233 PSVMANWIDVLKGEFFDISHRTTPFPSPVMSLFPPEQDLVMYFVAVSEYLFNTAGFV 292
QY 304 AGVLKMTLRDDMIKPKESKFLRTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQPTG 363
DB 293 AGALVFNLTDDMIKPKESSHLNTSSFGILLIPSIKMPNMLMKLISITASAPALNKP 352
QY 364 LTFYPAVDVQAFVLPNSLASLFLIGMHTTGSMEVSAESNRNLVGBELKDRLLLELKHN 423
DB 353 LTLSPVGNIQAVAILPNSLSLAPFLFLQLNTNVLAQVAVNSGKIIVSLELDKVEIQLVQSD 412
QY 424 TGPFPVELLDQIMNVIPLVLPVRYNEKLOKGFPLTPARVOLYNNVLOPHONFLIFGAD 483
DB 413 VGPFSVSLSTAVNYVVSATLLPVRYNEILKNGYPLIEHIIQLTDFVIQTYHYLLFGAN 472
QY 484 VVYK 487
DB 473 AHYE 476
```

```

RESULT 9
LBP_HUMAN
ID_LBP_HUMAN STANDARD; PRT; 481 AA.
AC P18428; Q43438; Q92672; Q9H403; Q9UD66;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DE Lipopolysaccharide-binding protein precursor (LBP).
GN Name=LBP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90385281; PubMed=2402637;
RA Schumann R.R., Leong S.R., Flagg G.W., Gray P.W., Wright S.D.,
RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
RT "Structure and function of lipopolysaccharide binding protein.";
RL Science 249:1429-1431(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292492; PubMed=7517398;
RA Wilde C.G., Seilhamer J.J., McGrogan M., Ashton N., Snable J.L.,
RA Lane J.C., Leong S.R., Thornton M.B., Miller K.L., Scott R.W.;
RT "Bactericidal/permeability-increasing protein and lipopolysaccharide
RT (LPS)-binding protein. LPS binding properties and effects on LPS-
RT mediated cell activation.";
RL J. Biol. Chem. 269:17411-17416(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Hubacek J.A., Aslanidis C., Schmitz G.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98110577; PubMed=9441745; DOI=10.1006/geno.1997.5030;
RA Kirschning C.J., Au-Young J., Lamping N., Reuter D., Pfeil D.,
RA Seilhamer J.J., Schumann R.R.;
RT "Similar organization of the lipopolysaccharide-binding protein (LBP)
RT and phospholipid transfer protein (PLTP) genes suggests a common gene
RT family of lipid-binding proteins.";
RL Genomics 46:416-425(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Long J.Y., Liu J.Q., Xue Y.N., Wang H.X.;
RT "Cloning and sequencing of human lipopolysaccharide-binding protein
RT gene.";
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 25:469-471(1998).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark A.P., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhali P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA LeHvaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,

```

```

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN [7]
RP SEQUENCE OF 1-41 FROM N.A.
RA Sutton C.L., Smith R.I.F., Centola M.B., Theofan G.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [8]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=98227852; PubMed=9568897;
RA Beamer L.J., Carroll S.F., Eisenberg D.;
RT "The BPI/LBP family of proteins: a structural analysis of conserved
RT regions.";
RL Protein Sci. 7:906-914(1998).
CC -I- FUNCTION: Binds to the lipid a moiety of bacterial
CC lipopolysaccharides (LPS), a glycolipid present in the outer
CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems
CC to interact with the CD14 receptor.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M35533; AAA59493.1; -
DR EMBL; X98657; CAA67226.1; -
DR EMBL; X98658; CAA67226.1; JOINED.
DR EMBL; X98659; CAA67226.1; JOINED.
DR EMBL; X98660; CAA67226.1; JOINED.
DR EMBL; X98661; CAA67226.1; JOINED.
DR EMBL; X98662; CAA67226.1; JOINED.
DR EMBL; X98663; CAA67226.1; JOINED.
DR EMBL; X98664; CAA67226.1; JOINED.
DR EMBL; X98665; CAA67226.1; JOINED.
DR EMBL; X98666; CAA67226.1; JOINED.
DR EMBL; X98667; CAA67226.1; JOINED.
DR EMBL; X98668; CAA67226.1; JOINED.
DR EMBL; AF013512; AAC39547.1; -
DR EMBL; AF013500; AAC39547.1; JOINED.
DR EMBL; AF013501; AAC39547.1; JOINED.
DR EMBL; AF013502; AAC39547.1; JOINED.
DR EMBL; AF013503; AAC39547.1; JOINED.
DR EMBL; AF013504; AAC39547.1; JOINED.
DR EMBL; AF013505; AAC39547.1; JOINED.
DR EMBL; AF013506; AAC39547.1; JOINED.
DR EMBL; AF013507; AAC39547.1; JOINED.
DR EMBL; AF013508; AAC39547.1; JOINED.
DR EMBL; AF013509; AAC39547.1; JOINED.
DR EMBL; AF013510; AAC39547.1; JOINED.
DR EMBL; AF013511; AAC39547.1; JOINED.
DR EMBL; AF105067; AAD21962.1; -
DR EMBL; AF105067; AAD21962.1; -
DR EMBL; AL080249; CAC10462.1; -
DR EMBL; L42172; AAA66446.1; -
DR PIR; A35843; A35843.
DR PIR; A54136; A54136.
DR HSPSP; P17213; IEFWF.
DR Genew; HGNC:6517; LBP.
DR MIM; 151990; -
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006953; P:acute-phase response; TAS.
DR GO; GO:0006968; P:cellular defense response; TAS.
DR GO; GO:0009618; P:response to pathogenic bacteria; TAS.
DR InterPro; IPR001124; LBP_BPI_CETP.

```

```
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
KW Antibiotic; Glycoprotein; Lipid transport; Signal; Transmembrane.
FT SIGNAL 1 25
FT CHAIN 26 481 Lipopolysaccharide-binding protein.
FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 386 386 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).
FT CONFLICT 6 6 R -> H (in Ref. 2).
FT CONFLICT 22 22 E -> C (in Ref. 2).
FT CONFLICT 82 82 N -> K (in Ref. 4).
FT CONFLICT 128 128 S -> F (in Ref. 4).
FT CONFLICT 154 157 VTAS -> GYCL (in Ref. 1).
FT CONFLICT 174 174 L -> S (in Ref. 1).
FT CONFLICT 257 257 R -> S (in Ref. 4).
FT CONFLICT 266 270 VMSLP -> A (in Ref. 1).
FT CONFLICT 369 369 L -> H (in Ref. 4).
FT CONFLICT 436 436 L -> F (in Ref. 2, 4 and 6).
SQ SEQUENCE 481 AA; 53349 MW; 81654B95E5E6864D0 CRC64;

Query Match 43.4%; Score 1088; DB 1; Length 481;
Best Local Similarity 44.8%; Pred. No. 4.4e-74;
Matches 210; Conservative 96; Mismatches 161; Indels 2; Gaps 2;

QY 18 LMVLVAIGTAVTAANPGVWVIRISOKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHL 77
DB 12 LLALLLTSTPEALGANPGVLARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIPIHV 71
QY 78 KGHYSFYSMDIREFQPSQISQSMVNVGLKFSISNANIKISGKWAQKRFKMGSGNFDL 137
DB 72 GGRYEFHSLNIHSCHELLHSALRPVPGQGLSLISDSISIRVQGRWKVRKSPFKLQSGSDV 131
QY 138 SIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHIKSKVGLWLIQHFHKKIESAL 197
DB 132 SVKGISISVNLILGSE-SSGRPTVTASSCSDIADVEVDM5-GDLGWLNLNLFHNQIESKF 189
QY 198 RNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYLGLVAPPATTATLTDVQMKG 257
DB 190 QKVLESRICEMIQKSVSDLOPYLQTLPTVTETIDSFADIDSLVBPATQMLEVFMFKG 249
QY 258 EYSENHNHPPFPAPVMEFFAAHDMRVYGLSDYFFNTAGIVYQAGVGLKMTLDDMIP 317
DB 250 EIFHRNHRSPVTLAAVMSLPPEHNKVVYFAISDVYFNTASLVYHEEGLNFSITDDMIP 309
QY 318 KESKRLTTKFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGLTFYPADVQAFV 377
DB 310 PDSNIRLTTSKFRPFVPRLARLYPNMNLQSGVSPAPLNFSPGNLSVDYPVELLDIMN 369
QY 378 LPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELKHGNIPIGPPVELLDIMN 437
DB 370 LPSSSKPEVFRLSVATNVSATLTFNTSKITGFKPKGVKVELKSKVGLFNALLEALLN 429
QY 438 YIVPILVLRVNEKLGKQGLPPLTPARVQLYNNVLOPHQNLFLFGADVY 486
DB 430 YIILNTLYPKFNKDLAEGFPLPLLRKQVLDLGLQLHKDFLFLGANVQY 478

RESULT 10
Q8TCF0 PRELIMINARY; PRT; 477 AA.
AC Q8TCF0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LBP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
```

```
RNA SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]
RNA SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022256; AAH22256.1; -.
DR HSSP; P17213; LEWF.
DR GO; GO:0008289; F:lipid binding; IEA.
DR InterPro; IPR001124; LBP_BPI_CETP.
DR Pfam; PF01273; LBP_BPI_CETP; 1.
DR Pfam; PF02886; LBP_BPI_CETP_C; 1.
DR SMART; SM00328; BPI1; 1.
DR SMART; SM00329; BPI2; 1.
DR PROSITE; PS00400; LBP_BPI_CETP; 1.
SQ SEQUENCE 477 AA; 52933 MW; 03D5E9D55A3BA6D0 CRC64;

Query Match 42.4%; Score 1062; DB 2; Length 477;
Best Local Similarity 44.6%; Pred. No. 4.2e-72;
Matches 205; Conservative 94; Mismatches 159; Indels 2; Gaps 2;

QY 18 LMVLVAIGTAVTAANPGVWVIRISOKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHL 77
DB 12 LLALLLTSTPEALGANPGVLARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIPIHV 71
QY 78 KGHYSFYSMDIREFQPSQISQSMVNVGLKFSISNANIKISGKWAQKRFKMGSGNFDL 137
DB 72 GGRYEFHSLNIHSCHELLHSALRPVPGQGLSLISDSISIRVQGRWKVRKSPFKLQSGSDV 131
QY 138 SIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHIKSKVGLWLIQHFHKKIESAL 197
DB 132 SVKGISISVNLILGSE-SSGRPTVTASSCSDIADVEVDM5-GDLGWLNLNLFHNQIESKF 189
QY 198 RNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYLGLVAPPATTATLTDVQMKG 257
DB 190 QKVLESRICEMIQKSVSDLOPYLQTLPTVTETIDSFADIDSLVBPATQMLEVFMFKG 249
QY 258 EYSENHNHPPFPAPVMEFFAAHDMRVYGLSDYFFNTAGIVYQAGVGLKMTLDDMIP 317
DB 250 EIFHRNHRSPVTLAAVMSLPPEHNKVVYFAISDVYFNTASLVYHEEGLNFSITDDMIP 309
QY 318 KESKRLTTKFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGLTFYPADVQAFV 377
DB 310 PDSNIRLTTSKFRPFVPRLARLYPNMNLQSGVSPAPLNFSPGNLSVDYPVELLDIMN 369
QY 378 LPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKDLRLLELKHGNIPIGPPVELLDIMN 437
DB 370 LPSSSKPEVFRLSVATNVSATLTFNTSKITGFKPKGVKVELKSKVGLFNALLEALLN 429
QY 438 YIVPILVLRVNEKLGKQGLPPLTPARVQLYNNVLOPHQNLFLFGADVY 477
```





Db	14	LSLLAARPGALGT--NPGLIITDKGLGLEYAAREGILLALQKLLVTLFDSGDGRK	70
Qy	76	HLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQK-R	127
Db	71	HFGRAQKFKYSLKIPRELLRGTURPLPGQGLSLDISDAIVHVRGSMKVKAFRLKNSF	130
Qy	136	DLSTEGHSIADLKLGNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLPHKKIES	187
Db	131	DLVYKGLTISVHLVLSGE-SGGRPTVTSSCSDIQNVELDI-EGDLEELNLLQSQIDA	188
Qy	196	ALRNKMSQVCEKVTNSVSSKLQYFOTLPVMTKIDSVAGINGLVAPPATTATLDDVM	255
Db	189	RLREVLSEKICRQIEBAVTAHLQYLQTLPTTQIDSFAGIDISLMEAPRATAGMLDMVF	248
Qy	256	KGEFYSNHNHNPFPAPPVMEFPAADRMVYLGSLDYFFNTAGLIVYOAGVLMKWLDDM	315
Db	249	KGEIFPLDHRSPVDFLAPAMNLPKASHRMVYFSDYVFNNTASLXHKSGVWNPFSITAM	308
Qy	316	IPKESKRLTTKFGTFLPEVAKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAF	375
Db	309	VPADLNIRRTTKSRFPVPLANLYPNNLQGVNSQLVNLSTENLLEEPEDMIEAL	368
Qy	376	AVLPNSSLASFLGMHTTGSMEVSAESNRLVGLKLDRLLELKHGNIQFPFVELLQDI	435
Db	369	VVLPSSAREPVRGLVATNVSATLITNTRKITGFKGRQLVGLKESKVGFGFVELLEAL	428
Qy	436	MNYITVPLVLPVNEKLOKFPPLTPARVOLYNNVLPQHNFLFGADVYK	487
Db	429	LNYYILNLYPKVNEKLAHRFPPLRLRHQIQLYDLLLQTHENFLVAGNIQVR	480
RESULT 14			
Qy	Q8JFX3	PRELIMINARY;	PRT; 473 AA.
AC	Q8JFX3		
DT	01-OCT-2002	(Tremblrel. 22, Created)	
DT	01-OCT-2002	(Tremblrel. 22, Last sequence update)	
DE	01-OCT-2003	(Tremblrel. 25, Last annotation update)	
DE	LBP	(LPS binding protein)/BPI (Bactericidal/permeability-increasing protein) like-2.	
GN	Name=LBP/BPI-2;		
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
OX	NCBI_TaxID=8022;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22018144; PubMed=12023361;		
RA	Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,		
RA	Nakanishi T., Yokomizo Y., Soma G.;		
RT	"Cloning and characterization of the homolog of mammalian		
RT	lipopolysaccharide-binding protein and bactericidal permeability-		
RT	increasing protein in rainbow trout Oncorhynchus mykiss.";		
RL	J. Immunol. 168:5638-5644(2002).		
DR	EMBL; AB042026; BAB91244.1; -.		
DR	HSSP; P17213; 1EMF.		
DR	GO; GO:0008289; F:lipid binding; IEA.		
DR	InterPro; IPR001124; LBP_BPI_CETP.		
DR	Pfam; PF01273; LBP_BPI_CETP_1.		
DR	Pfam; PF02886; LBP_BPI_CETP_C; 1.		
DR	SMART; SM00328; BPI1; 1.		
DR	SMART; SM00329; BPI2; 1.		
SQ	SEQUENCE 473 AA; 51262 MW; 00977A492EB09920 CRC64;		
Query Match 34.7%; Score 870.5; DB 2; Length 473;			
Best Local Similarity 35.3%; Pred. No. 1.5e-57;			
Matches 169; Conservative 121; Mismatches 178; Indels 11; Gaps 6;			
Qy	9	PCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDY	68
Db	3	PC-----CLLALLAV-ISLTLAASPGVKVKLTDKGIEYKQIGWASLQKLTWKVPDL	55
RESULT 15			
Qy	Q8JFX4	PRELIMINARY;	PRT; 473 AA.
AC	Q8JFX4		
DT	01-OCT-2002	(Tremblrel. 22, Created)	
DT	01-OCT-2002	(Tremblrel. 22, Last sequence update)	
DT	01-OCT-2003	(Tremblrel. 25, Last annotation update)	
DE	LBP	(LPS binding protein)/BPI (Bactericidal/permeability-increasing protein)-1.	
GN	Name=LBP/BPI-1;		
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
OX	NCBI_TaxID=8022;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22018144; PubMed=12023361;		
RA	Inagawa H., Honda T., Kohchi C., Nishizawa T., Yoshiura Y.,		
RA	Nakanishi T., Yokomizo Y., Soma G.;		
RT	"Cloning and characterization of the homolog of mammalian		
RT	lipopolysaccharide-binding protein and bactericidal permeability-		
RT	increasing protein in rainbow trout Oncorhynchus mykiss.";		
RL	J. Immunol. 168:5638-5644(2002).		
DR	EMBL; AB042025; BAB91243.1; -.		
DR	HSSP; P17213; 1EMF.		
DR	GO; GO:0008289; F:lipid binding; IEA.		
DR	InterPro; IPR001124; LBP_BPI_CETP.		
DR	Pfam; PF01273; LBP_BPI_CETP_1.		
DR	Pfam; PF02886; LBP_BPI_CETP_C; 1.		
DR	SMART; SM00328; BPI1; 1.		
DR	SMART; SM00329; BPI2; 1.		
SQ	SEQUENCE 473 AA; 51430 MW; 3F9DF180695CA3D7 CRC64;		
Query Match 34.6%; Score 867.5; DB 2; Length 473;			
Best Local Similarity 35.1%; Pred. No. 2.5e-57;			
Matches 168; Conservative 119; Mismatches 181; Indels 11; Gaps 6;			
Qy	9	PCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAALQKELKRIKIPDY	68
Db	3	PC---CWALLALVFF-----ALATNPGVKVKLTGKIEYKQIGWASLQKLTWKVPDL	55
Qy	69	SDSPFKHLKKGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWAQ-KR	127

Db	56	SGTERVAPIGVKYSLTGITIVNIGLPSALALVPTGISLSITNAFISLHGNWKIRYLS	115
Qy	128	FLKMSGNFDLSIEGMSISADIKLGSNPTSGKPTITCSCSSHINSVHVHISKSVGWLIQ	187
Db	116	FIKOSGSDLEVDGLTVDSITIKSDET-GRPTVSSVNCVANVGSASIKP-HGGASWLYN	173
Qy	188	LFHKKIESALRNKMSQVCEKVTNSVSKLQPYFQTLFVMTKIDSVAGINYGLVAPPATT	247
Db	174	LFSAYIDKALRSALQKQICPLVADTITD-MNPHLKTNLVLAKVDKYAEVEYSMTVPTIS	232
Qy	248	AETLDVQMKGEFYSENHHNPPFPAPVMEFPAADHDMVYLGSDYFFNTAGLVYQACVL	307
Db	233	NASIDFSLKGEFYNIKGHEPFPSPFSLPQVNNMLYIGMSAFTTNSAGFVYNNAGAL	292
Qy	308	KWTLRDDMI PKESKFRLTTPKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFY	367
Db	293	SLYITDDMIPSSPIRLNTRTFGAFIPEIAKRFPSMMKLVKTVKTEIFFEPNNVTQ	352
Qy	368	PAVDVQAFVLPNSLASLFLIGHMTTGSMEVSASERNLVGELKLDRLLELKHNSIGPF	427
Db	353	ASGVTAYAIQPNITLSPFLVLMSEGSVARSLYVTGVRLAGAVTLNKIEMTLETSYVGQF	412
Qy	428	PVELLDIMNIVIPILVLPVNEKLQGFPLPTPARVOLYNNVLQPHQNFLLFGADVY	486
Db	413	QVRSILDNIFLWLVKVAVIPKNARLEKGFPLPSIGKMNLVNTQLQVLKDYMLIGTDVQF	471

Search completed: October 21, 2005, 11:30:48  
Job time : 174.285 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:43 ; Search time 14.2593 Seconds  
(without alignments)  
1241.566 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193  
Perfect score: 943  
Sequence: 1 CNAPRWWSMLVLAIGTAVT.....RVHISKVKGWLIQLFHKKI 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	487	A30909	bactericidal/permeability-increasing protein precursor - human
2	832	88.2	250	A43383	bactericidal/permeability-increasing protein precursor - human
3	596.5	63.3	482	S10180	bactericidal/permeability-increasing protein precursor - human
4	430	45.6	481	A51136	lipopolysaccharide
5	428	45.4	481	I56246	lipopolysaccharide
6	416	44.1	477	A35843	lipopolysaccharide
7	357.5	37.9	482	B35843	lipopolysaccharide
8	172.5	18.3	493	I49370	plasma phospholipid
9	169	17.9	493	A35333	phospholipid trans
10	130.5	13.8	493	A28941	cholesterol ester
11	129.5	13.7	497	I46692	cholesterol ester
12	120.5	12.8	493	A53176	cholesterol ester
13	110	11.7	576	T22700	hypothetical protein
14	102	10.8	606	T23190	hypothetical protein
15	98.5	10.4	824	E87856	protein F10D11.6
16	98.5	10.4	846	T20710	hypothetical protein
17	95	10.1	488	C86183	hypothetical protein
18	92	9.8	464	T16889	hypothetical protein
19	90.5	9.6	486	T20482	hypothetical protein
20	89	9.4	827	D96907	phage-related protein
21	84.5	9.0	1169	G72571	probable DNA-direct
22	84	8.9	405	D84871	probable polygalactonate
23	82.5	8.7	498	B99946	hypothetical protein
24	82.5	8.7	573	S50627	hypothetical protein
25	82.5	8.7	218	B84683	hypothetical protein
26	82	8.7	554	T15438	hypothetical protein
27	82	8.7	1120	T38431	DNA-directed RNA p
28	81.5	8.6	1902	C97702	cell surface antigen
29	80	8.5	440	B71162	hypothetical protein

30	79.5	8.4	518	2	S73432	MG096 homolog D09-
31	79.5	8.4	869	2	T22422	hypothetical prote
32	79.5	8.4	1134	2	T04587	hypothetical prote
33	78.5	8.3	433	2	T03632	ornithine decarbox
34	78.5	8.3	2154	2	P83068	hypothetical prote
35	78	8.3	201	2	AG2778	conserved hypotet
36	78	8.3	201	2	C97558	hypothetical prote
37	78	8.3	274	2	T51714	probable formamido
38	78	8.3	390	2	E96565	hypothetical prote
39	78	8.3	390	2	T51713	probable formamido
40	78	8.3	766	2	S61424	inorganic diphosph
41	77.5	8.2	373	2	E90241	soluble hydrogenas
42	77.5	8.2	473	2	S17448	probable ligand-bi
43	77.5	8.2	999	2	F72453	probable cytochrom
44	77	8.2	439	2	H71413	probable cucumisin
45	77	8.2	571	2	T12773	conserved hypotet

## ALIGNMENTS

RESULT 1  
A30909  
bactericidal/permeability-increasing protein precursor - human  
N:Alternate names: SSK bactericidal protein

C:Species: Homo sapiens (man)  
C:Date: 18-Apr-1989 #sequence revision 18-Apr-1989 #text-change 09-Jul-2004  
C:Accession: A33850; B54136; A29464; A43600; A49716; A30909  
R:Gray, P.W.; Flagg, G.; Leong, S.R.; Gumina, R.J.; Weiss, J.; Ooi, C.E.; Elsbach, P.  
J. Biol. Chem. 264, 9505-9509, 1989  
A:Title: Cloning of the cDNA of a human neutrophil bactericidal protein. Structural and  
A:Reference number: A33850; MUID:89255455; PMID:2722846  
A:Accession: A33850  
A:Molecule type: mRNA  
A:Residues: 1-487 <GRA>  
A:Cross-references: UNIPROT:Q9UCT4; GB:J04739; NID:gl79528; PID:AA51841.1; PID:gl79529  
R:Wilde, C.G.; Seilheimer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A:Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-bindi  
A:Reference number: A54136; MUID:94292492; PMID:7517398  
A:Accession: B54136  
A>Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-374, 'L', 376-487 <WIL>  
A:Experimental source: HL-60 cells  
A>Note: sequence extracted from NCBI backbone (NCBI:149855)  
R:Ooi, C.E.; Weiss, J.; Elsbach, P.; Frangione, B.; Mannion, B.  
J. Biol. Chem. 262, 14891-14894, 1987  
A:Title: A 25-Kda amino-terminal fragment carries all the antibacterial activities of th  
A:Reference number: A29464; MUID:88033057; PMID:3667613  
A:Accession: A29464  
A:Molecule type: protein  
A:Residues: 32-51 <OOI>  
A:Experimental source: neutrophils  
R:Wasilik, K.R.; Skubitz, K.M.; Gray, B.H.  
Infect. Immun. 59, 4193-4200, 1991  
A:Title: Comparison of granule proteins from human polymorphonuclear leukocytes which ar  
A:Reference number: A43600; MUID:92040097; PMID:1937776  
A:Accession: A43600  
A:Molecule type: protein  
A:Residues: 32-52, 'R' <WAS>  
R:Little, R.G.; Kainer, D.N.; Lim, E.; Burke, D.J.; Conlon, P.J.  
J. Biol. Chem. 269, 1865-1872, 1994  
A:Title: Functional domains of recombinant bactericidal/permeability increasing protein  
A:Reference number: A49716; MUID:94124531; PMID:8294435  
A:Accession: A49716  
A:Molecule type: protein  
A:Residues: 32-130, 132-141, 143-165, 202-215, 'E', 217-225 <LIT>  
C:Comment: The bactericidal/permeability-increasing protein (BPI) is a 60 kD membrane-as  
which is specific for gram-negative bacteria. BPI has a high affinity for lipopolysaccha  
between BPI and an LPS-binding protein from liver and cholesterol ester transfer protein  
C:Genetics:  
A:Gene: GDB:BPI

A;Cross-references: GDB:131572; OMIM:109195  
A;Map Position: 20q11.23-20q12  
C;Superfamily: lipopolysaccharide-binding protein  
C;Keywords: antibacterial; cytotoxin; glycoprotein; heparin binding; neutrophil  
F;1-31/Domain: signal sequence #status predicted <SIG>  
F;32-487/Product: bactericidal permeability-increasing protein #status predicted <MAT>  
F;32-51/Region: bactericidal #status predicted  
F;380/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 943; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1e-77;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 60  
DB 10 CNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 69  
QY 61 DPFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 120  
DB 70 DPFKIKHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 129  
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLF 180  
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLF 189  
QY 181 HKKI 184  
DB 190 HKKI 193

RESULT 2  
S43383  
bactericidal/permeability-increasing protein - synthetic  
C;Species: synthetic  
A;Title: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C;Date: 20-Oct-1994 #sequence\_revision 15-Feb-1996 #text\_change 15-Feb-1996  
C;Accession: S43383  
R;Qi, S.Y.; Li, Y.; O'Connor, C.D.  
Biochem. J. 298, 711-718, 1994  
A;Title: The region around residue 115 of human bactericidal/permeability-increasing protein of a gene coding for the active domain and characterization of recombinant proteins.  
A;Reference number: S43383  
A;Accession: S43383  
A;Molecule type: DNA  
A;Residues: 1-250 <QIS>

Query Match 88.2%; Score 832; DB 4; Length 250;  
Best Local Similarity 100.0%; Pred. No. 5.4e-68;  
Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 VNPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDMIRE 82  
DB 2 VNPGVVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSDFKIKHLGKHGHSFYSDMIRE 61  
QY 83 FQLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKL 142  
DB 62 FQLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDLSIEGMSISADLKL 121  
QY 143 SNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 184  
DB 122 SNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 163

RESULT 3  
S10180  
bactericidal permeability-increasing protein precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10180  
R;Leong, S.R.; Camerato, T.  
Nucleic Acids Res. 18, 3052, 1990  
A;Title: Nucleotide sequence of the bovine bactericidal permeability increasing protein  
A;Reference number: S10180; MUID:90272418; PMID:2349103

A;Accession: S10180  
A;Molecule type: mRNA  
A;Residues: 1-482 <LEO>  
A;Cross-references: UNIPROT:P17453; EMBL:X52563; NID:g138; PIDN:CAA36797.1; PID:g139  
C;Superfamily: lipopolysaccharide-binding protein  
F;1-26/Domain: signal sequence #status predicted <SIG>  
F;27-482/Product: bactericidal permeability increasing protein #status predicted <MAT>

Query Match 63.3%; Score 596.5; DB 2; Length 482;  
Best Local Similarity 63.2%; Pred. No. 2.8e-46;  
Matches 115; Conservative 29; Mismatches 37; Indels 1; Gaps 1;

QY 3 APRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYS 62  
DB 8 ARRWATLVLAALGTAVT-TTNGEIVARITQGLDYACQGVLTQLKELEKTIIPNPSGN 66  
QY 63 FKIHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 122  
DB 67 FKIHLGKHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRF 126  
QY 123 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFH 182  
DB 127 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFH 186  
QY 183 KI 184  
DB 187 RI 188

RESULT 4  
A54136  
lipopolysaccharide-binding protein - human  
N;Alternate names: LBP; LPS-binding protein  
C;Species: Homo sapiens (man)  
C;Date: 11-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A54136  
R;Wilde, C.G.; Seilhamer, J.J.; McGrogan, M.; Ashton, N.; Snable, J.L.; Lane, J.C.; Leon  
J. Biol. Chem. 269, 17411-17416, 1994  
A;Title: Bactericidal/permeability-increasing protein and lipopolysaccharide (LPS)-binding protein  
A;Accession: A54136  
A;Reference number: A54136; MUID:94292492; PMID:7517398  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-481 <WIL>  
A;Cross-references: UNIPROT:P18428  
A;Experimental source: liver  
A;Note: sequence extracted from NCBI backbone (NCBIP:149401)  
C;Superfamily: lipopolysaccharide-binding protein

Query Match 45.6%; Score 430; DB 2; Length 481;  
Best Local Similarity 46.6%; Pred. No. 3.5e-31;  
Matches 82; Conservative 38; Mismatches 54; Indels 2; Gaps 2;

QY 9 LMVLVAIGTAVTAANPGVVRISQKGLDYASQOQTAAALQKELKRIKIPDYSFKIKHL 68  
DB 12 LLALLTSTPCALGANFGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRPHV 71  
QY 69 GKHHGHSFYSDMIREFOLPSSQISMPVNVGLKFSISNANIKISGKWAQKRFKMSGNFDL 128  
DB 72 GRGRYEFHSLNIHSCHELLSALRPVPGQGLSLSDSSIRVQGRWKVKRFFKLQGSFDV 131  
QY 129 SIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKVGWLIQLFHKKI 184  
DB 132 SVKGISISVNLGLQSP-SSGRPTVTASSCSDIADVEVDMS-GDLGLWLLNLFHNQI 185

RESULT 5  
I56246  
lipopolysaccharide binding protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I56246  
R;Su, G.L.; Freeswick, P.D.; Geller, D.A.; Wang, Q.; Shapiro, R.A.; Wan, Y.H.; Billiar, J.

J. Immunol. 153, 743-752, 1994  
A:Title: Molecular cloning, characterization, and tissue distribution of rat lipopolysaccharide-binding protein (LBP)  
A:Reference number: I56246; MUID:94292804; PMID:8021509  
A:Accession: I56246  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-481 <RES>  
A:Cross-references: UNIPROT:Q63313; GB:I32132; NID:g510714; PIDN:AAA21835.1; PID:g510715  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 45.4%; Score 428; DB 2; Length 481;  
Best Local Similarity 44.2%; Pred. No. 5.4e-31;  
Matches 80; Conservative 45; Mismatches 5; Indels 2; Gaps 2;  
Qy 4 PRWSLMVLVAIGTAVTAANVPGVVIRISQKGLDYASQOGTAALQKELKRIKIPDYSDF 63  
Db PLLPTLLGLLLSIPRTQGNPAMVVRITDKGLEVAAKEGLLSLQRELYKKITLPDFSGDF 66  
Qy 64 KIKHLGKHYSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGWKAQKFLKMS 123  
Db KIKAVRGQYEFHSLIEQSCQLRGSLLKPLPGRGLSLISDSSISVGRKWKVRRSFVKLH 126  
Qy 124 GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGMWLIOLEPHKK 183  
Db GSFDLVKSVTIISVDLLGLGVDP-SERPVTAGCSNRIIDLELHVS-GNVGMLLNFHQ 184  
Qy 184 I 184  
Db 185 I 185

RESULT 6  
A35843  
lipopolysaccharide-binding protein - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004  
C:Accession: A35843  
R:Schumann, R.R.; Leong, S.R.; Flagg, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T  
Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; MUID:90385281; PMID:2402637  
A:Accession: A35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-477 <SCH>  
A:Cross-references: UNIPROT:P18428; GB:M35533; NID:g186965; PIDN:AAA59493.1; PID:g186968  
C:Genetics:  
A:Gene: GDB:LBP  
A:Cross-references: GDB:I31571; OMIM:151990  
A:Map position: 20q11.23-20q12  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 44.1%; Score 416; DB 2; Length 477;  
Best Local Similarity 46.0%; Pred. No. 6.5e-30;  
Matches 81; Conservative 36; Mismatches 57; Indels 2; Gaps 2;  
Qy 9 LMVLVAIGTAVTAANVPGVVIRISQKGLDYASQOGTAALQKELKRIKIPDYSDFKIKHL 68  
Db LLALLTSTPEALGANPGLVARITDKGLQYAAQEGLLALQSELLRITLPDFTGDLRIPHV 71  
Qy 69 KGKHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGWKAQKFLKMSGNFL 128  
Db GRGRYEFHSLNHSCELLHSALRPVPGQGLSLISDSSIRVQGRKWKVRRSFVKLGSFV 131  
Qy 129 STEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGMWLIOLEPHKKI 184  
Db SVKGISISVLLLGSE-SSGRPTGYCLSCSSDIADVEVDMGDS-GWLLNLFHQI 185

RESULT 7  
B35843  
lipopolysaccharide-binding protein - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 05-Oct-1990 #sequence\_revision 05-Oct-1990 #text\_change 09-Jul-2004  
C:Accession: B35843; A46553  
R:Schumann, R.R.; Leong, S.R.; Flagg, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; T  
Science 249, 1429-1431, 1990  
A:Title: Structure and function of lipopolysaccharide binding protein.  
A:Reference number: A35843; MUID:90385281; PMID:2402637  
A:Accession: B35843  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-482 <SCH>  
A:Cross-references: UNIPROT:P17454; GB:M35534; NID:g165467; PIDN:AAA9235.1; PID:g165468  
R:Tobias, P.S.; Soldau, K.; Ulevitch, R.J.  
J. Exp. Med. 164, 777-793, 1986  
A:Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru  
A:Reference number: A46553; MUID:86306528; PMID:2427635  
A:Accession: A46553  
A:Molecule type: protein  
A:Residues: 27-55, 'XG', 58-62, 'P', 64-65 <TOB>  
C:Superfamily: lipopolysaccharide-binding protein  
C:Keywords: acute phase

Query Match 37.9%; Score 357.5; DB 2; Length 482;  
Best Local Similarity 41.0%; Pred. No. 1.3e-24;  
Matches 73; Conservative 39; Mismatches 61; Indels 5; Gaps 3;  
Qy 7 VSLMVLVAIGTAVTAANVPGVVIRISQKGLDYASQOGTAALQKELKRIKIPDYSDFKIK 66  
Db LSLLLAAAPGALGT---NPGLITRITDKGLEVAAREGLLALQKLELVLPDSDGDFRIK 70  
Qy 67 HLGRGHYSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGWKAQKFLKMSGNF 126  
Db HFGRAQYKFSYSLKIPRFELLGRTLPFGQGLSLDISDAYIHVRGSKVRKAFRLKMSF 130  
Qy 127 DLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKVGMWLIOLEPHKKI 184  
Db DLYVGLGLTISVHLVLGSE-SSGRPTVTTCSSSDIQNVELDI-EGDLELLNLLSQI 186

RESULT 8  
I49370  
plasma phospholipid transfer protein - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49370  
R:Albers, J.J.; Wolfbauer, G.; Cheung, M.C.; Day, J.R.; Ching, A.F.; Lok, S.; Tu, A.Y.  
Biochim. Biophys. Acta 1258, 27-34, 1995  
A:Title: Functional expression of human and mouse plasma phospholipid transfer protein.  
A:Reference number: I49370; MUID:95383401; PMID:7654777  
A:Accession: I49370  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-493 <RES>  
A:Cross-references: UNIPROT:P55065; EMBL:U37226; NID:g1051265; PIDN:AAA80542.1; PID:g1051265  
C:Superfamily: lipopolysaccharide-binding protein

Query Match 18.3%; Score 172.5; DB 2; Length 493;  
Best Local Similarity 28.8%; Pred. No. 8.4e-08;  
Matches 47; Conservative 40; Mismatches 63; Indels 13; Gaps 4;  
Qy 9 LMVLVAIGTAVTAANV---PGVVIRISQKGLDYASQOGTAALQKELKRIKIPDYSDFKI 65  
Db MYLLWALFLALLAGAHAEPLPGCKIRVTSAAALDLVKQEGRLFLEQLETTITPDV----- 54  
Qy 66 KHLGKHYSFYSDMIR--EFPQLPSQISWPNVGLKFSISNANIKISGWKAQKFLKMS 123  
Db YGAKGHFYNYISDVRTVQLHLISSELHFQPDQDLLLLNISNLASGLHFRQLLYWFLYDG 113  
Qy 124 GNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHV 166  
Db GYINASAEVSIKRTGLQL-SQDSSGRKIVSNVSCBASVSKMM 155

RESULT 9

A53533  
phospholipid transfer protein precursor - human  
N:Alternate names: lipid transfer protein II; PLTP  
C:Species: Homo sapiens (man)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 09-Jul-2004  
C:Accession: A53533  
E:Day, J.R.; Albers, J.J.; Lofton-Day, C.E.; Gilbert, T.L.; Ching, A.F.T.; Grant, F.J.;  
J. Biol. Chem. 269, 9388-9391, 1994  
A:Title: Complete cDNA encoding human phospholipid transfer protein from human endothelial  
A:Reference number: A53533; MUID:94179366; PMID:8132678  
A:Accession: A53533  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-493 <DAY>  
A:Cross-references: UNIPROT:P55058; GB:L26232; NID:G468325; PIDN:AAA36443.1; PID:G468326  
C:Genetics:  
A:Gene: GDB:PLTP  
A:Cross-references: GDB:340911; OMIM:172425  
A:Map position: 20pter-20qter  
C:Superfamily: lipopolysaccharide-binding protein  
C:Keywords: glycoprotein; phosphoprotein  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-493/Product: phospholipid transfer protein #status experimental <MAT>

Query Match 17.9%; Score 169; DB 2; Length 493;  
Best Local Similarity 28.7%; Pred. No. 1.8e-07;  
Matches 41; Conservative 32; Mismatches 60; Indels 10; Gaps 3;

Qy 25 PGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYSDFKIKHLGKGH--YSFYSDMIRE 82  
Db 20 PGCKIRTVSKALELVKQEGRLFQELETITIPDLRGK-----EGHFFYNISEVKVTE 72

Qy 83 FQLPSSQISVMVNVGLKFSISNANIKISGKWAQKRLKMSGNFDLSIEGWSADLKLK 142  
Db 73 LQLTSSSELDFOQOQELMLQITNASLGRFRRLQLLYWFYDGGYINAGSGVIRTGLELS 132

Qy 143 SNPTSGKPTTICSSCSHINSVH 165  
Db 133 RDP-AGRMKYSNVSCASVSRMH 154

RESULT 10  
A26941  
cholesteryl ester transfer protein precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 09-Jul-2004  
C:Accession: A26941  
E:Drayna, D.; Jarnagin, A.S.; McLean, J.; Henzel, W.; Kohr, W.; Fielding, C.; Lawn, R.  
Nature 327, 632-634, 1987  
A:Title: Cloning and sequencing of human cholesteryl ester transfer protein cDNA.  
A:Reference number: A26941; MUID:87258172; PMID:3600759  
A:Accession: A26941  
A:Molecule type: mRNA  
A:Residues: 1-493 <DR>  
A:Cross-references: UNIPROT:P11597; EMBL:M30185; NID:g180259; PIDN:AAA51977.1; PID:g180259  
C:Genetics:  
A:Gene: GDB:CE7P  
A:Cross-references: GDB:119773; OMIM:118470  
A:Map position: 16q13-16q13  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-493/Product: cholesteryl ester transfer protein #status predicted <MAT>

Query Match 13.8%; Score 130.5; DB 2; Length 493;  
Best Local Similarity 21.9%; Pred. No. 0.00055;  
Matches 40; Conservative 40; Mismatches 90; Indels 13; Gaps 5;

Qy 8 SLMLVLVAIGTAVTAIV-----NPGVVVRISQKGLDYASQOGTAALQKELKRIKIPDYSDF 63  
Db 5 TVTLTALLGNHAHACKGTSHEAGIVCRITKPAALLVLAHETAKVIQTAFQASVYPDITGEK 64

Qy 64 KIKHLGKHGYFSYNDIREFQLPSSQISVMVNVGLKFSISNANIKISGKWK---AQKRFL 120  
Db 65 AMMLILGVKYGKLNITQISLSTASSQVLEFAKSIDVSIQNSVSVKGTIKYGYTTAWML 124



**This Page Blank (uspto)**

Page 2-15 all work

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:38 ; Search time 170.559 Seconds  
(without alignments)  
1104.324 Million cell updates/sec

Title: US-10-629-516-2

Perfect score: 2507

Sequence: 1 MRENARGPCNAPRWWSLMV.....NVVLQPHNQLFLGADVVK 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2507	100.0	487	1 AAU06198	Human bac
2	2507	100.0	487	2 AAR44420	Human bac
3	2507	100.0	487	2 AAR62370	Recombina
4	2507	100.0	487	2 AAR57901	Bacterici
5	2507	100.0	487	2 AAR62344	Recombina
6	2507	100.0	487	2 AAR68923	Bacterici
7	2507	100.0	487	2 AAR79185	Recombina
8	2507	100.0	487	2 AAR79021	Bacterici
9	2507	100.0	487	2 AAR81247	Recombina
10	2507	100.0	487	2 AAR80995	Bacterici
11	2507	100.0	487	2 AAR67998	Holoprote
12	2507	100.0	487	2 AAR86455	rBPI for
13	2507	100.0	487	2 AAR76243	Recombina
14	2507	100.0	487	2 AAR05852	Recombina
15	2507	100.0	487	2 AAR97568	Human bac
16	2507	100.0	487	2 AAW17987	Bacterici
17	2507	100.0	487	2 AAW44550	Human bac
18	2507	100.0	487	2 AAW01702	Human bac
19	2507	100.0	487	2 AAW17986	Human bac
20	2507	100.0	487	2 AAW47090	Human bac
21	2507	100.0	487	2 AAW40141	Human rec
22	2507	100.0	487	2 AAW61158	Recombina
23	2507	100.0	487	2 AAW56156	A bacteri
24	2507	100.0	487	2 AAW26776	Human bac
25	2507	100.0	487	2 AAW63306	Recombina

ALIGNMENTS

RESULT 1

AAU06198	2507	100.0	487	2	AAW63304	Human bac
XX	2507	100.0	487	2	AAW41359	Human bac
XX	2507	100.0	487	2	AAW94284	Human bac
XX	2507	100.0	487	2	AAV17864	Human bac
XX	2507	100.0	487	2	AAV31621	Human bac
XX	2507	100.0	487	2	AAV26930	Recombina
XX	2507	100.0	487	2	AAV98885	Human bac
XX	2507	100.0	487	3	AAV51169	Human BPI
XX	2507	100.0	487	3	AAV88382	Human bac
XX	2507	100.0	487	3	AAV16109	Human bac
XX	2507	100.0	487	3	AAV16184	Recombina
XX	2507	100.0	487	3	AAV68319	Human bac
XX	2507	100.0	487	3	AAV03943	Bacterici
XX	2507	100.0	487	3	AAV18762	A human b
XX	2507	100.0	487	3	AAV07751	A human b
XX	2507	100.0	487	3	AAV11117	Human BPI
XX	2507	100.0	487	3	AAV13335	Human BPI
XX	2507	100.0	487	4	AAV09357	Human rBP
XX	2507	100.0	487	4	AAV97625	Human BPI
XX	2507	100.0	487	4	AAV01016	Recombina

AAU06198 standard; protein; 487 AA.

AAU06198;

16-JAN-2002 (first entry)

Human bactericidal/permeability-increasing (BPI) protein.

Human; bactericidal permeability-increasing protein; BPI; PMN;

polymorphonuclear leukocyte; Gram-negative bacteria; bacteraemia; sepsis;

bacterial infection; skin infection; decubitus ulcer; burn; vulnerary;

antimicrobial; antibacterial; immunosuppressive; protein therapy.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..31

Protein 32..487

Protein /label= Mature\_BPI\_protein

US6287811-B1.

11-SEP-2001.

10-MAY-1999; 99US-00309217.

11-AUG-1987; 87US-00084335.

05-AUG-1988; 88US-00228035.

17-SEP-1991; 91US-00762730.

11-DEC-1991; 91US-00805031.

22-JAN-1993; 93US-00007837.

23-JAN-1995; 95US-00361299.

(UJNY ) UNIV NEW YORK STATE.

Elasbach P, Weiss J;

WPI; 1989-068849/09.

N-PSDB; AAS13679.

Bactericidal-permeability increasing holoprotein fragments - used for

treatment of diseases caused by gram-negative bacteria such as

bacteraemia or sepsis.

Example 5; Fig 5A-D; 20pp; English.

XX CC The present invention relates to the isolation of human  
CC bactericidal/permeability-increasing (BPI) protein from polymorphonuclear  
CC leukocytes (PMN). BPI can be produced by growing in a culture medium,  
CC host cells transformed or transfected to express BPI encoded by  
CC nucleotides 124-1491 of the BPI polynucleotide sequence or its  
CC complementary strand, or a human BPI DNA sequence that hybridizes under  
CC stringent hybridization conditions with the BPI polynucleotide sequence  
CC or its complementary strand. BPIs are useful against a wide range of Gram  
CC -negative bacteria, particularly for the treatment of diseases caused by  
CC Gram-negative bacteria such as bacteraemia or sepsis, infections caused  
CC by Escherichia coli, Salmonella, Klebsiella or Pseudomonas, and skin  
CC infections which occur in bedridden patients suffering from decubitus  
CC ulcers (bed sores) or in burn patients. They can also be used as a model  
CC for the design of new antibiotic agents, to provide sequence information  
CC on BPI to direct the design of future generations of antimicrobial agents  
CC specific for Gram-negative bacteria, and to be used as probes in  
CC molecular biological techniques. The BPI protein sequence is also useful  
CC in protein therapy. The present sequence represents the human BPI protein  
CC of the present invention  
XX CC  
SQ Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 1; Length 487;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60  
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHNSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240  
Qy 241 VAPPATTAETLDVQMGGEFSENNHNPFPAPPVMEFPAAHDMVYLGLSDYFNTAGLV 300  
Db 241 VAPPATTAETLDVQMGGEFSENNHNPFPAPPVMEFPAAHDMVYLGLSDYFNTAGLV 300  
Qy 301 YQEAGVLKMTLRDDMIPKESKFRITTKFFGTFLPEVAKFPNKKIQIHVSASTPPHLSVQ 360  
Db 301 YQEAGVLKMTLRDDMIPKESKFRITTKFFGTFLPEVAKFPNKKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTTFPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGBELKLRLLLELK 420  
Db 361 PTGLTTFPAVDVQAFVLPNSSLASLFLIGHMTTGSMEVSAESNRLVGBELKLRLLLELK 420  
Qy 421 HSNIGPPFVELLDIMNVIYPIVLPRVNEKLGKGFPLPTPARVOLNVLQPHQNFLLF 480  
Db 421 HSNIGPPFVELLDIMNVIYPIVLPRVNEKLGKGFPLPTPARVOLNVLQPHQNFLLF 480  
Qy 481 GADVYVK 487  
Db 481 GADVYVK 487

RESULT 2  
AAR44420

ID AAR44420 standard; protein; 487 AA.

XX AC AAR44420;

XX DT 25-MAR-2003 (revised)

DT 03-JUN-1994 (first entry)

XX

DE DE PING4512 encoded fusion protein.  
XX  
XX Polymerase chain reaction; primer; amplify; PCR; plasmid; PING4512;  
KW PING4503; bactericidal/permeability-increasing protein; BPI; IgG; heavy;  
KW chain; pMB27; fusion protein; Gram negative; renal failure;  
KW bacterial infection; endotoxin related shock; metabolic acidosis;  
KW disseminated intravascular coagulation; anemia; thrombocytopenia;  
KW leukopenia; adult respiratory distress syndrome; hypotension; fever;  
KW constant region; lipopolysaccharide complement binding;  
KW placental transfer; Fc receptor binding.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FT Peptide 1..31 "Signal peptide"  
FT Protein 32..487  
FT /note= "Mature rBPI (191) -IgG fusion protein"  
XX  
XX WO9323434-A2.  
XX  
XX 25-NOV-1993.  
XX  
XX 19-MAY-1993; 93WO-US004754.  
XX  
XX 19-MAY-1992; 92US-00885911.  
XX  
XX (XOMA ) XOMA CORP.  
XX  
XX Theofan G, Grinna LS, Horwitz A;  
PI  
XX  
XX WPI; 1993-386485/48.  
XX N-PSDB; AAQ52488.  
XX  
XX New fusion proteins for treating bacterial infections - comprising a  
PT bactericidal-permeability-increasing protein and an immunoglobulin heavy  
PT chain constant domain.  
XX  
XX Claim 20; Page 48-50; 75pp; English.  
XX  
XX This sequence is encoded by the plasmid PING4512. PING4512 was  
CC constructed using the primer sequence given in AAQ52480. Plasmid PING4503  
CC was cut with AlwNI, the ends made blunt with T4 DNA polymerase, and the  
CC DNA then cut with SalI. The resultant approx. 700bp SalI/blunt fragment  
CC contains the 30 bp 5' untranslated region and the DNA encoding the signal  
CC peptide and first 191 amino acids of bactericidal/permeability-increasing  
CC protein (BPI). IgG heavy chain (HC) sequences, which also included the  
CC hinge region of the IgG HC were PCR amplified from plasmid pMB27 using  
CC these primers. Plasmids such as PING4512 may be used to produce fusion  
CC proteins which are useful for the treatment of Gram negative bacterial  
CC infections and their sequelae including endotoxin related shock and  
CC conditions associated with it, such as disseminated intravascular  
CC coagulation, anemia, thrombocytopenia, leukopenia, adult respiratory  
CC distress syndrome, renal failure, hypotension, fever and metabolic  
CC acidosis. Providing BPI or a fragment of it, as part of the fusion with an  
CC immunoglobulin heavy chain constant region provides the potential  
CC advantages of Fc receptor binding, bivalent binding to lipopoly-  
CC saccharide complement binding and increasing placental transfer. (Updated  
CC on 25-MAR-2003 to correct FN field.)  
XX  
SQ Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60

Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRSQKGLDYASQGGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISG 120



QY 121 KWKAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWKAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPYFQTLPMVTKIDSVAGINYL 240  
 DB 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPYFQTLPMVTKIDSVAGINYL 240  
 QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 QY 301 YQEAGVLKMTLRDDMI PKESFRLTTPKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQEAGVLKMTLRDDMI PKESFRLTTPKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 DB 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLGKGFPLTPARVQLNVNVLQPHONFLF 480  
 DB 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLGKGFPLTPARVQLNVNVLQPHONFLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487

RESULT 3  
 AAR62370  
 ID AAR62370 standard; protein; 487 AA.  
 AC AAR62370;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 27-APR-1995 (first entry)  
 XX  
 DE Recombinant bactericidal/permeability-increasing protein (rBPI-50).  
 KW N-terminal; recombinant; bactericidal/permeability protein; rBPI;  
 KW signal protein; human; rBPI-23; binding assay; heparin-binding; domain;  
 KW Limulus amoebocyte lysate; LAL; inhibition; bactericidal activity;  
 KW chronic inflammatory disease; arthritis; psoriasis; Crohn's disease;  
 KW inflammatory bowel disease; asthma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Location/Qualifiers  
 FT Peptide  
 FT 1..31  
 FT /note= "Signal peptide"  
 FT Domain  
 FT 17..55  
 FT /note= "LAL inhibiting domain"  
 FT Binding-site  
 FT 21..55  
 FT /note= "Heparin binding site"  
 FT Protein  
 FT 32..487  
 FT /note= "mature protein"  
 FT Binding-site  
 FT 65..107  
 FT /note= "Heparin binding site"  
 FT Domain  
 FT 73..99  
 FT /note= "LAL inhibiting domain"  
 FT Active-site  
 FT 85..99  
 FT /note= "Bactericidally active fragment"  
 FT Binding-site  
 FT 137..171  
 FT /note= "Heparin binding site"  
 FT Domain  
 FT 137..163  
 FT /note= "LAL inhibiting domain"  
 XX  
 PN WO9420128-A1  
 XX  
 PD 15-SEP-1994.  
 XX

PF 11-MAR-1994; 94WO-US002401.  
 XX  
 PR 12-MAR-1993; 93US-00030644.  
 PR 15-JUL-1993; 93US-00093202.  
 XX  
 PA (XOMA ) XOMA CORP.  
 XX  
 FI Little RG, Gazzanosantoro H, Parent JB;  
 XX  
 DR WPI; 1994-302679/37.  
 DR N-PSDB; AAQ73382.  
 XX  
 XX Uses of bactericidal permeability increasing protein product - to  
 FT neutralise anticoagulant effect of heparin, to inhibit angiogenesis or  
 FT cell proliferation, as contraceptive and to reduce inflammation.  
 XX  
 PS Disclosure; Page 43-45; 78pp; English.  
 XX  
 CC This sequence represents the N-terminal of recombinant bactericidal/  
 CC permeability (rBPI) protein. This expression product encoding the 31  
 CC residue signal protein and the first 199 amino acids of the N-terminal of  
 CC mature human BPI has a molecular weight of 23 kD and is designated rBPI-  
 CC 23. In binding assays rBPI-23 was shown to have three separate functional  
 CC domains with heparin-binding activity, at least three major domains with  
 CC significant Limulus amoebocyte lysate (LAL) inhibition and one region  
 CC with bactericidal activity. BPI, or active fragments of it may be used to  
 CC treat and prevent the effects of chronic inflammatory disease states such  
 CC as arthritis, psoriasis, inflammatory bowel disease, Crohn's disease and  
 CC asthma. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-  
 CC 2003 to correct PI field.)  
 XX

SQ Sequence 487 AA;

Query Match 100.0%; Score 2507; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred No. 4.3e-229;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQKGLDYASQQTAAQLKEL 60  
 DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVGVVVRISQKGLDYASQQTAAQLKEL 60  
 QY 61 KRIKIPYSDSFKIKHKGHYFSYMDIRFOLPSSQISMVNVNGLKFSISNANIKISG 120  
 DB 61 KRIKIPYSDSFKIKHKGHYFSYMDIRFOLPSSQISMVNVNGLKFSISNANIKISG 120  
 QY 121 KWKAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWKAQKFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPYFQTLPMVTKIDSVAGINYL 240  
 DB 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSKLPYFQTLPMVTKIDSVAGINYL 240  
 QY 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 DB 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEPPAAHDMVYLGLSDYFFNTAGLV 300  
 QY 301 YQEAGVLKMTLRDDMI PKESFRLTTPKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQEAGVLKMTLRDDMI PKESFRLTTPKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 DB 361 PTGLTFFPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLGKGFPLTPARVQLNVNVLQPHONFLF 480  
 DB 421 HSNIGPPFVELLDIMNVIIVPLVLPVNEKLGKGFPLTPARVQLNVNVLQPHONFLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487

```

RESULT 4
AAR57901
ID AAR57901 standard; protein; 487 AA.
XX
XX AAR57901;
AC
XX 25-MAR-2003 (revised)
DT 29-MAR-1995 (first entry)
DT
XX
XX Bactericide BPI.
DE
XX
XX BPI; bactericidal-permeability-increasing protein; bactericide;
KW fusion protein; Gram-negative bacterium; infection.
KW
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1. .31
FT /label= Sig_peptide
XX
XX WO9418323-A1.
PN
XX
XX 18-AUG-1994.
PD
XX
XX 02-FEB-1994; 94WO-US001235.
PF
XX
XX 02-FEB-1993; 93US-00013801.
PR
XX
XX (XOMA ) XOMA CORP.
PA
XX
XX Theofan G, Horwitz A, Burke D, Baltaian M, Grinna L;
PI
XX
XX WPI; 1994-279744/34.
DR N-PSDB; AAQ67270.
DR
XX
XX Bactericidal-permeability-increasing protein analogues with Cys132 or
PT Cys135 replaced - also fusion proteins and C-terminally truncated forms,
PT have increased stability and are useful to treat gram-negative bacterial
PT infection.
XX
XX Disclosure; Page 52-54; 77pp; English.
PS
XX
XX Analogs, fusion proteins and C-terminal truncated forms of human BPI are
CC claimed that show improved resistance to dimerization and adduct
CC formation. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 487 AA;
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229; Mismatches 0; Gaps 0;
Matches 487; Conservative 0; Indels 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVVRISQKGLDYASQGGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVVRISQKGLDYASQGGTAALQKEL 60
Qy 61 KRKIPDYSDFKIKHLGKGHSFYSDMDIREFQLPSSQISNMPNVNGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHSFYSDMDIREFQLPSSQISNMPNVNGLKFSISNANIKISG 120
Qy 121 KWKAKQKFLKMGNGFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHLSKS 180
Db 121 KWKAKQKFLKMGNGFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHLSKS 180
Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVNVSVKLQPYFQTLPVMTKIDSVAGINYGL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVNVSVKLQPYFQTLPVMTKIDSVAGINYGL 240
Qy 241 VAPPATTAAETLDVQMKGEFSENHHNPPPPAPPVMEFPAADRNVYGLSDYDFNTAGLV 300
Db 241 VAPPATTAAETLDVQMKGEFSENHHNPPPPAPPVMEFPAADRNVYGLSDYDFNTAGLV 300

```

---

```

QY 301 YQEAGVLKMTLRDDMIKESKFRLLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMIKESKFRLLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTFYPADVQAFVLPNSSIASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSIASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420
QY 421 HSNIGPFPVELLDIMNYIVPILVLPVNEKLOKGPPLTPARVOLYNNVVLQPHQNFLLF 480
Db 421 HSNIGPFPVELLDIMNYIVPILVLPVNEKLOKGPPLTPARVOLYNNVVLQPHQNFLLF 480
QY 481 GADVVK 487
Db 481 GADVVK 487

RESULT 5
AAR62344
ID AAR62344 standard; protein; 487 AA.
XX
XX AAR62344;
AC
XX 25-MAR-2003 (revised)
DT 02-MAY-1995 (first entry)
DT
XX
XX Recombinant 23 kD human BPI N-terminal protein.
DE
XX
XX BPI; bactericidal/permeability-increasing protein; rBPI23; therapy;
KW treatment; infection; Mycobacteria; leprosy; tuberculosis; LAM;
KW lipoarabinomannan; improved pulmonary clearance; gram negative;
KW pneumonia model.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1. .31
FT /label= signal_sequence
FT Protein 32. 487
FT /label= N-terminus_ of_human_BPI_holo_protein
XX
XX WO9420129-A1.
PN
XX
XX 15-SEP-1994.
PD
XX
XX 11-MAR-1994; 94WO-US002463.
PF
XX
XX 12-MAR-1993; 93US-00031145.
PR
XX
XX (XOMA ) XOMA CORP.
PA
XX
XX Lambert LH;
PI
XX
XX WPI; 1994-302680/37.
DR N-PSDB; AAQ72017.
DR
XX
XX Treating Mycobacterium infections with bactericidal-permeability inducing
PT peptide - also used for in vivo and in vitro neutralisation of
PT mycobacterial lipoarabinomannan.
XX
XX Disclosure; Page 21-23; 35pp; English.
PS
XX
XX AAR62344 shows the recombinant 23 kD, 199 amino acid residue amino-
CC terminal fragment of human BPI (bactericidal/permeability-increasing
CC protein) holoprotein referred to as rBPI23. The sequence given is taken
CC from Grey et al., and varies to that from Gazzano-Santoro et al. In the
CC latter, the valine at position 141 is specified by GTG rather than GTC
CC and residue 185 is glutamic acid (specified by GAG) rather than lysine
CC (specified by AAG). The expression vector also encodes for a 31 residue
CC signal sequence. rBPI23 or biologically active deriva. are useful in the
CC treating of a subject suffering from any of the physiological effects of
CC LAM (lipoarabinomannan) from Mycobacteria. (Updated on 25-MAR-2003 to
CC correct PN field.)

```

```

XX SQ Sequence 487 AA;
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229; Mismatches 0; Indels 0; Gaps 0;
Matches 487; Conservative 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQTAAALQKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQTAAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISMVNVNGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISMVNVNGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSLSASFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTTFYPAVDVQAFVLPNSLSASFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPPPEVLLQDIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480
Db 421 HSNIGPPPEVLLQDIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 6
AAR68923
ID AAR68923 standard; protein; 487 AA.
XX AC AAR68923;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 11-SEP-1995 (first entry)
XX DE Bactericidal/permeability-increasing protein (rBPI).
XX KW Lipopolysaccharide binding protein; rLPS; LPS; BPI;
XX KW gram-negative bacterial infections; treatment;
XX KW bactericidal/permeability-increasing protein.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..32
XX FT /label= sig_peptide
XX FN W09500641-A1.
XX PD 05-JAN-1995.
XX XX
XX PF 17-JUN-1994; 94WO-US006931.
XX PR 17-JUN-1993; 93US-00079510.
XX XX

```

```

PA (XOMA ) XOMA CORP.
XX Gazzano-Santoro H, Theofan G, Trown PW;
XX WPI; 1995-052078/07.
XX DR N-PSDB; AAQ80827.
XX PT binding protein deriv. and hybrid protein binds to lipo:polysaccharide -
XX PT lacks CD14-mediated immuno-stimulatory properties, used to treat Gram-
XX PT negative bacterial infections and associated conditions.
XX PS Example 2; Page 70-72; 11app; English.
XX CC AAQ80827 encodes AAR68923 recombinant bactericidal/permeability-
XX CC increasing protein (rBPI). The protein contains the lipopolysaccharide
XX CC (LPS) binding domain fragments described in AAR68919-R68921. The
XX CC fragments are used in the construction of hybrid proteins for the
XX CC treatment gram-negative bacterial infections and associated conditions.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 487 AA;
Query Match 100.0%; Score 2507; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.3e-229; Mismatches 0; Indels 0; Gaps 0;
Matches 487; Conservative 0;

Qy 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQTAAALQKEL 60
Db 1 MRENWARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQQTAAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISMVNVNGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLGKGHSYFSDIREFQLPSSQISMVNVNGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNQSVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADHDMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAADHDMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLTTFKFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSLSASFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTTFYPAVDVQAFVLPNSLSASFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420

Qy 421 HSNIGPPPEVLLQDIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480
Db 421 HSNIGPPPEVLLQDIMNYIVPILVLRVNEKLGKGFPLPTPARVOLYNNVLOPHQNFLLF 480

Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 7
AAR79185
ID AAR79185 standard; protein; 487 AA.
XX AC AAR79185;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 21-DEC-1995 (first entry)
XX DE Recombinant bactericidal/permeability-increasing protein rBPI.

```

```

XX Bactericidal/permeability-increasing protein; BPI; endotoxin;
KW Gram negative bacteria.
XX
XX Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal
XX
XX WO9519784-A1.
XX
XX 27-JUL-1995.
XX
XX 24-JAN-1995; 95WO-US001151.
XX
XX 24-JAN-1994; 94US-00180221.
XX 16-AUG-1994; 94US-00291112.
XX
XX (XOMA ) XOMA CORP.
XX
XX Friedmann N, Scannon PJ, Van Deventer SJH, Von Der Mohlen MAM,
XX Wedel N;
XX
XX WPI; 1995-269271/35.
XX N-PSDB; AAQ97483.
XX
XX Treatment of humans exposed to bacterial endotoxin in circulation - using
XX bactericidal/permeability-increasing protein product to alleviate
XX increase in circulating tumour necrosis factor and interleukin 6.
XX
XX Disclosure; Page 43-45; 60pp; English.
XX
XX Bactericidal/permeability-increasing protein (BPI) is a protein extracted
XX from the granules of mammalian polymorphonuclear neutrophils. The mol.
XX wt. of the entire human BPI protein is approx. 55,000 daltons. The AA
XX sequence of the entire human BPI protein, as well as the DNA encoding the
XX protein, have been elucidated in Figure 1 of Gray et al., J. Biol. Chem.
XX 264:9505 (1989) and are incorporated by reference. In Gazzano-Santoro et
XX al., Infect. Immun. 60:4754-4761 (1992) an expression vector was used as
XX a source of DNA encoding a recombinant expression product (rBPI23) having
XX the 31- residue signal sequence and the first 199 AAs of the N-terminus
XX of the mature human BPI, as set out in Figure 1 of Gray et al., except
XX that Val151 is specified by GTG rather than GTC, and residue 185 is Glu
XX (specified by GAG) rather than Lys (specified by AAG). Recombinant
XX holoprotein (rBPI) has also been produced having the sequence
XX (AAQ97483/R79185) set out in Figure 1 of Gray et al., with the exceptions
XX noted for rBPI23 and the exception that residue 417 is Ala (specified
XX by GCT) rather than Val (specified by GTT). In the spec., the BPI protein
XX product is used for the treatment of humans exposed to bacterial
XX endotoxin in circulation. BPI protein products are administered in dosage
XX ants. of 0.1-10 mg/kg body wt. by parenteral routes. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
XX Sequence 487 AA;
XX
XX Query Match 100.0%; Score 2507; DB 2; Length 487;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-229;
XX Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKEL 60
XX |||||
XX 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQGTAALQKEL 60
XX
XX 61 KRKIPDYSDFKIKHLKGHYSPYMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
XX |||||
XX 61 KRKIPDYSDFKIKHLKGHYSPYMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120
XX
XX 121 KWAQAKRFLKQSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSHHNSVHVHISKS 180
XX |||||
XX 121 KWAQAKRFLKQSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSHHNSVHVHISKS 180
XX
XX 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPVFQTLPVMTKIDSVAGINYGL 240
XX |||||
XX
XX 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPVFQTLPVMTKIDSVAGINYGL 240
XX |||||
XX
XX 241 VAPPATTATETLDVQMKGEFYSENHNHPPFPAPPVMEFPAAHDRMVYLGSLSDYFNTAGLV 300
XX |||||
XX 241 VAPPATTATETLDVQMKGEFYSENHNHPPFPAPPVMEFPAAHDRMVYLGSLSDYFNTAGLV 300
XX |||||
XX
XX 301 YOEAGVLKMTLRDDMIPEKSKPRLTTKFTGTFLEPAVAKKFPNNMKIQIHVSASTPPHLSVQ 360
XX |||||
XX 301 YOEAGVLKMTLRDDMIPEKSKPRLTTKFTGTFLEPAVAKKFPNNMKIQIHVSASTPPHLSVQ 360
XX |||||
XX
XX 361 PTGLTFYPADVQAFVAVLNPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
XX |||||
XX 361 PTGLTFYPADVQAFVAVLNPNSLASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
XX |||||
XX
XX 421 HSNIGFPVELLQDINNYIVPILVLPVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480
XX |||||
XX 421 HSNIGFPVELLQDINNYIVPILVLPVNEKLOKGFPLPTPARVQLYNVVVLQPHQNFLLF 480
XX |||||
XX
XX 481 GADVYK 487
XX |||||
XX
XX 481 GADVYK 487
XX
XX RESULT 8
XX AAR79021
XX ID AAR79021 standard; protein; 487 AA.
XX
XX AAR79021;
XX
XX 25-MAR-2003 (revised)
XX
XX 25-JAN-1996 (first entry)
XX
XX Bactericidal/permeability increasing protein.
XX
XX Bactericidal permeability increasing protein; BPI; infection; control;
XX recombinant.
XX
XX Homo sapiens.
XX
XX US5439807-A.
XX
XX 08-AUG-1995.
XX
XX 19-MAY-1993; 93US-00072063.
XX
XX 19-MAY-1992; 92US-00885501.
XX
XX (XOMA ) XOMA CORP.
XX
XX Grinna LS;
XX
XX WPI; 1995-283094/37.
XX N-PSDB; AAQ97607.
XX
XX Recovery of recombinant endotoxin binding protein - by culturing
XX transformed cells in medium contg. cation exchange material, useful for
XX treatment of bacterial infections.
XX
XX Example 1; Col 13-16; 18pp; English.
XX
XX Recombinant endotoxin-binding protein comprising bactericidal/
XX permeability increasing protein (BPI) or its endotoxin N-terminal
XX fragment, can be produced by growing genetically transformed host cells
XX in a suitable medium so that BPI is secreted into the medium. The BPI
XX is then isolated and can be used to control bacterial infections.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 487 AA;
XX
XX Query Match 100.0%; Score 2507; DB 2; Length 487;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-229;
XX Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVRISQKGLDYASQOQTAALQKEL 60  
 DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVRISQKGLDYASQOQTAALQKEL 60  
 QY 61 KRIKIPDYSDFSFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120  
 DB 61 KRIKIPDYSDFSFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120  
 QY 121 KWAKQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWAKQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDSVAGINYL 240  
 DB 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDSVAGINYL 240  
 QY 241 VAPPATTATLTVQMGKGFYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300  
 DB 241 VAPPATTATLTVQMGKGFYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300  
 QY 301 YQAGVLMKMTLRDDMI PKESKFRLLTKFPGTLPVAKKFPNMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQAGVLMKMTLRDDMI PKESKFRLLTKFPGTLPVAKKFPNMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSABNSRLVGLKLDRLLELK 420  
 DB 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSABNSRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLDQIMNVIPTLVPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
 DB 421 HSNIGPPFVELLDQIMNVIPTLVPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487  
 RESULT 9  
 AAR81247  
 ID AAR81247 standard; protein; 487 AA.  
 XX AC AAR81247;  
 XX DT 18-MAR-1996 (first entry)  
 XX DE Recombinant bactericidal/permeability increasing holoprotein.  
 XX KW Bactericidal/permeability increasing protein; BPI; granule; mammalian;  
 KW polymorphonuclear neutrophil; anti-bacterial; fungus; infection; ss;  
 KW antifungal; fluconazole; amphotericin B; Candida albicans; sterilise;  
 KW lipopolysaccharide binding protein; protein; sterilisation; medical instrument.  
 XX OS Synthetic.  
 XX FH Key  
 FT Peptide 1..31 Location/Qualifiers  
 FT Peptide /note= "signal peptide"  
 FT Peptide 32..487  
 FT Peptide /note= "mature peptide"  
 XX W09519179-A1.  
 XX 20-JUL-1995.  
 XX 13-JAN-1995; 95WO-US000498.  
 XX 14-JAN-1994; 94US-00183222.  
 PR 11-MAR-1994; 94US-00209762.  
 PR 11-JUL-1994; 94US-00273540.  
 XX (XOMA ) XOMA CORP.  
 XX

PI Little RG, Lim E, Scannon PJ, Lambert LH;  
 XX WPI; 1995-263713/34.  
 DR N-PSDB; AAQ99816.  
 XX  
 PT Treating fungal infection with bactericidal permeability increasing  
 PT protein or deriv. - esp. for control of systemic Candida albicans  
 PT infection or for use in in vitro sterilisation.  
 XX  
 PS Example 1; Page 105-107; 153pp; English.  
 XX  
 CC The amino acid sequence of a recombinant bactericidal/permeability  
 CC increasing (BPI) protein. BPI protein can be isolated from the granules  
 CC of mammalian polymorphonuclear neutrophils (PMN). The protein has  
 CC antibacterial activity associated with 3 functional domains: I  
 CC (AAR81085), II (AAR81086) and III (AAR81087) present in N-terminal region  
 CC of the BPI holoprotein (AAR81245). The antibacterial regions were used to  
 CC design the antifungal peptides AAR81083-4, AAR81088-R81244 and AAR81248-  
 CC R81308. The peptides are used to treat fungal infections together with  
 CC other antifungal cpds e.g. fluconazole or amphotericin B. The antifungal  
 CC activity of the peptides may also be enhanced by addition of a  
 CC lipopolysaccharide binding protein (LBP) e.g. AAR81246. The peptides can  
 CC be used to treat fungal infection, esp. Candida albicans. They are also  
 CC useful for killing or inhibiting fungi in vitro e.g. for sterilising  
 CC medical instruments  
 XX  
 SQ Sequence 487 AA;  
 Query Match 100.0%; Score 2507; DB 2; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-229; Indels 0; Gaps 0;  
 Matches 487; Conservative 0; Mismatches 0;  
 QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVRISQKGLDYASQOQTAALQKEL 60  
 DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVPGVVRISQKGLDYASQOQTAALQKEL 60  
 QY 61 KRIKIPDYSDFSFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120  
 DB 61 KRIKIPDYSDFSFKIKHLKGHYSPYMDIREPQLPSSQISWPNVGLKFSINANIKISG 120  
 QY 121 KWAKQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 DB 121 KWAKQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
 QY 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDSVAGINYL 240  
 DB 181 KVGWLIQLFHHKIESALRNKMSQVCEKVTNSVSSKLOPYFQTLPMVKIDSVAGINYL 240  
 QY 241 VAPPATTATLTVQMGKGFYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300  
 DB 241 VAPPATTATLTVQMGKGFYSENHNPPPPFAPVMEFPAADRMVYLGSDYFFNTAGLV 300  
 QY 301 YQAGVLMKMTLRDDMI PKESKFRLLTKFPGTLPVAKKFPNMKIQIHVSASTPPHLSVQ 360  
 DB 301 YQAGVLMKMTLRDDMI PKESKFRLLTKFPGTLPVAKKFPNMKIQIHVSASTPPHLSVQ 360  
 QY 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSABNSRLVGLKLDRLLELK 420  
 DB 361 PTGLTFYPADVQAFVLPNSLSLFLIGMHTTGSMEVSABNSRLVGLKLDRLLELK 420  
 QY 421 HSNIGPPFVELLDQIMNVIPTLVPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
 DB 421 HSNIGPPFVELLDQIMNVIPTLVPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLLF 480  
 QY 481 GADVYK 487  
 DB 481 GADVYK 487  
 RESULT 10  
 AAR80995  
 ID AAR80995 standard; protein; 487 AA.  
 XX

AC AAR80995;  
XX DT 23-MAY-1996 (first entry)  
XX Bactericidal/permeability increasing protein (rBPI).  
XX bactericidal/permeability increasing peptide; BPI; heparin; binding;  
KW neutralisation; lipopolysaccharide; LPS; bactericidal activity;  
KW treatment; neutralise endotoxin; inhibit angiogenesis;  
KW inhibit tumour formation; proliferation.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH Peptide 1..31  
FT /label= Signal\_peptide  
FT Protein 32..487  
FT /label= mature\_peptide  
XX WO9519372-A1.  
PN 20-JUL-1995.  
XX 15-SEP-1994; 94WO-US010427.  
XX 14-JAN-1994; 94US-00183222.  
PR 11-MAR-1994; 94US-00209762.  
XX (XOMA ) XOMA CORP.  
XX Little RG;  
XX WPI; 1995-263828/34.  
DR N-PSDB; AAT00951.  
XX New peptide(s) based on bactericidal/permeability-increasing protein -  
PT having heparin binding and neutralisation, LPS binding and neutralisation  
PT and antimicrobial activities.  
XX Disclosure; Page 147-150; 275pp; English.  
XX Recombinant bactericidal/permeability increasing protein (rBPI) is  
CC encoded by AAT00951. BPI (bactericidal permeability-increasing) peptides  
CC (AAR80996-81081 and AAR82553-372) each have an amino acid sequence that  
CC is deriv. of a BPI functional domain (or a variant) having at least one  
CC of the biological activities of BPI, such as heparin binding or  
CC neutralisation; lipopolysaccharide (LPS) binding or neutralisation or  
CC bactericidal activity. The BPI peptides are based on the amino-terminal  
CC portion of BPI, esp. functional domains I, II, and III (BPI residues 17-  
CC 45, 65-99 and 142-169 resp.)  
XX Sequence 487 AA;  
Query Match 100.0%; Score 2507; DB 2; Length 487;  
Best Local Similarity 100.0%; Pred. No. 4.3e-229; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0;  
Qy 1 MRENARGPCNAPRWVSLMWLVLAIGTAVTAANFVGVVVRISQKGLDYASQGGTAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMWLVLAIGTAVTAANFVGVVVRISQKGLDYASQGGTAALQKEL 60  
Qy 61 KRIKIPDYSDFKIKHLKGHSYFSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120  
Db 61 KRIKIPDYSDFKIKHLKGHSYFSDMDIREFQLPSSQISMPVNVGLKFSISNANIKISG 120  
Qy 121 KWKAKQKFLKMGNFDSLIEGMSISADLKLSNPTSGKPTITCSSSHNSVHVHISKS 180  
Db 121 KWKAKQKFLKMGNFDSLIEGMSISADLKLSNPTSGKPTITCSSSHNSVHVHISKS 180  
Qy 181 KVGWLIQLFHHKIESALRNKNSQVCEKVTNSVSKLPYFQTLFVMTKIDSVAGINYL 240  
Db 181 KVGWLIQLFHHKIESALRNKNSQVCEKVTNSVSKLPYFQTLFVMTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPPPFAPPVMEFPAAHDMRWYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPPPFAPPVMEFPAAHDMRWYLGLSDYFFNTAGLV 300  
Qy 301 YQEAGVLKMTLRDDMIPKESKFLRTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
Db 301 YQEAGVLKMTLRDDMIPKESKFLRTTKFFGTFLPEVAKFPNNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPADVQAFVLPNSSLASLFLQGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPADVQAFVLPNSSLASLFLQGMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPVELLDIMNYIVPILVLRVNEKLGKGFPLPTPARVQLYNVVYLQPHQNFLLF 480  
Db 421 HSNIGPPVELLDIMNYIVPILVLRVNEKLGKGFPLPTPARVQLYNVVYLQPHQNFLLF 480  
Qy 481 GADVVK 487  
Db 481 GADVVK 487  
RESULT 11  
AAR67998  
ID AAR67998 standard; protein; 487 AA.  
XX  
AC AAR67998;  
XX 25-MAR-2003 (revised)  
DT 15-AUG-1995 (first entry)  
XX Homo sapiens.  
XX Bactericidal/permeability-increasing protein; BPI; rBPI; rBPI50;  
KW lipopolysaccharide binding protein; LBP; rLBP25; rLBP;  
KW Gram-negative bacterium; infection; antiseptic.  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..31  
FT /label= Sig\_peptide  
FT Peptide 32..487  
FT /label= Mat\_peptide  
FT /note= "rBPI50 holoprotein"  
XX WO9502414-A1.  
PN 26-JAN-1995.  
XX 13-JUL-1994; 94WO-US007834.  
XX 14-JUL-1993; 93US-00093201.  
PR 11-JUL-1994; 94US-00274303.  
XX (XOMA ) XOMA CORP.  
XX Horwitz A;  
XX WPI; 1995-067161/09.  
DR N-PSDB; AAQ81445.  
XX Method for treating gram negative bacterial infection - comprises  
PT administering lipopolysaccharide binding protein (LBP) prod. and  
FT bactericidal/permeability-increasing (BPI) protein prod.  
XX Disclosure; Page 36-38; 76pp; English.  
XX Gram-negative bacterial infections are treated by co-administration of  
CC BPI protein and LBP. Recombinant BPI 50 kDa holoprotein rBPI50 (given in  
CC AAR67998) is the preferred BPI. (Updated on 25-MAR-2003 to correct PN  
CC field.)  
XX Sequence 487 AA;

XX	Query Match	100.0%;	Score 2507;	DB 2;	Length 487;
XX	Best Local Similarity	100.0%;	Pred. No. 4.3e-229;		
XX	Matches 487;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
PT	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRI	SQKGLDYASQGGTAALQKEL	60	
PT	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRI	SQKGLDYASQGGTAALQKEL	60	
XX	61	KRIKIPDYSDSFKIKHLGKGHYSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISG	120		
XX	61	KRIKIPDYSDSFKIKHLGKGHYSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISG	120		
XX	121	KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS	180		
XX	121	KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS	180		
XX	181	KVGWLIQLFHKIKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPVMTKIDSVAGINYGL	240		
XX	181	KVGWLIQLFHKIKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPVMTKIDSVAGINYGL	240		
XX	241	VAPPATTATLTDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMRVYLGSLDYFFNTAGLV	300		
XX	241	VAPPATTATLTDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMRVYLGSLDYFFNTAGLV	300		
XX	301	YQEAGVLKMTLRDDMI	PKESKFLRTTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360	
XX	301	YQEAGVLKMTLRDDMI	PKESKFLRTTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360	
XX	361	PTGLTFYPADVQAFAPVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK	420		
XX	361	PTGLTFYPADVQAFAPVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK	420		
XX	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLQKGFPLTPARVQLYNNVLPQHONFLF	480		
XX	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLQKGFPLTPARVQLYNNVLPQHONFLF	480		
XX	481	GADVVYK	487		
XX	481	GADVVYK	487		
XX	RESULT 12				
XX	AAR86455				
XX	ID AAR86455	standard; protein; 487 AA.			
XX	AC AAR86455;				
XX	DT 15-MAR-1996	(first entry)			
XX	DE rBPI	for use in treating liver damage.			
XX	BPI; bactericidal permeability increasing protein; RES;				
XX	KW reticuloendothelial; Kupffer cells; liver insult; hepatotoxic;				
XX	KW hepatectomy; trauma; viral hepatitis; chronic inflammatory.				
XX	Synthetic.				
XX	Key	Location/Qualifiers			
XX	FT Protein	32..487			
XX	FT /label=	rBPI			
XX	WO9510297-A1.				
XX	20-APR-1995.				
XX	05-OCT-1994;	94WO-US011404.			
XX	15-OCT-1993;	93US-00132510.			
XX	(XOMA )	XOMA CORP.			
XX	PI Van Leeuwen PA,	Boermeester MA;			

XX	WPI; 1995-161572/21.			
XX	Use of bactericidal/permeability-increasing protein prods. - for treating			
XX	adverse physiological effects of a depressed reticuloendothelial system			
XX	function.			
XX	Claim 6, 13; Page 42, 43; 136pp; English.			
XX	The patent relates to the new use of a BPI protein product for treating			
XX	adverse effects associated with depressed reticuloendothelial system			
XX	function, especially diminished function of Kupffer cells of the liver			
XX	resulting from physical, chemical or biological insult. Physical insult			
XX	is exemplified by partial or total hepatectomy such as accompanies			
XX	transplantation, and trauma. Chemical insult is exemplified by the			
XX	results of exposure to hepatotoxic substances such as chloroform,			
XX	glucosamine, carbon tetrachloride and ethanol. Biological insult is			
XX	exemplified by (non-)infectious diseases such as viral hepatitis and			
XX	chronic inflammatory hepatitis. The BPI protein product is preferably			
XX	rBPI-23, rBPI-21, rBPI, rBPI-42 dimer or one of 222 specified BPI			
XX	peptides. The present sequence is that of rBPI			
XX	Sequence 487 AA;			
XX	Query Match 100.0%; Score 2507; DB 2; Length 487;			
XX	Best Local Similarity 100.0%; Pred. No. 4.3e-229;			
XX	Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0			
Qy	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRI	SQKGLDYASQGGTAALQKEL	60
Db	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVVRI	SQKGLDYASQGGTAALQKEL	60
Qy	61	KRIKIPDYSDSFKIKHLGKGHYSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISG	120	
Db	61	KRIKIPDYSDSFKIKHLGKGHYSFYSDIREFQLPSSQISMPVNVGLKFSISNANIKISG	120	
Qy	121	KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS	180	
Db	121	KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS	180	
Qy	181	KVGWLIQLFHKIKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPVMTKIDSVAGINYGL	240	
Db	181	KVGWLIQLFHKIKIESALRNKNMSQCEKVTNSVSSKLPQYFQTLPVMTKIDSVAGINYGL	240	
Qy	241	VAPPATTATLTDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMRVYLGSLDYFFNTAGLV	300	
Db	241	VAPPATTATLTDVQMGGEFYSENHNPPFPAPPVMEFFAAHDMRVYLGSLDYFFNTAGLV	300	
Qy	301	YQEAGVLKMTLRDDMI	PKESKFLRTTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360
Db	301	YQEAGVLKMTLRDDMI	PKESKFLRTTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360
Qy	361	PTGLTFYPADVQAFAPVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK	420	
Db	361	PTGLTFYPADVQAFAPVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEKLDRLLELK	420	
Qy	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLQKGFPLTPARVQLYNNVLPQHONFLF	480	
Db	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLQKGFPLTPARVQLYNNVLPQHONFLF	480	
Qy	481	GADVVYK	487	
Db	481	GADVVYK	487	
XX	RESULT 13			
XX	AAR76243			
XX	ID AAR76243	standard; protein; 487 AA.		
XX	AC AAR76243;			
XX	DT 01-FEB-1996	(first entry)		
XX				

DE	Recombinant BPI holoprotein.		
XX	BPI peptide; bacterial permeability-increasing peptide; bactericidal;		
KW	therapeutic effectiveness; antibiotic; concurrent administration;		
KW	reverse resistance; gram-negative bacteria.		
XX	Homo sapiens.		
OS			
XX			
PH	Key	Location/Qualifiers	
FT	Peptide	1. .31	
FT	/note= "signal peptide"		
FT	Protein	32. .487	
FT	/note= "mature recombinant BPI"		
XX	WO9508344-A1.		
XX	30-MAR-1995.		
XX	22-SEP-1994;	94WO-US011225.	
XX	22-SEP-1993;	93US-00125651.	
PR	11-JUL-1994;	94US-00273401.	
XX	(XOMA ) XOMA CORP.		
PA	Cohen J, Kung AHC, Lambert LH, Little RG;		
XX	WPI; 1995-161465/21.		
DR	N-PSDB; AAQ92640.		
XX	BPI protein and an antibiotic in a medicament - for treatment of gram-		
PT	negative bacterial infection.		
XX	Disclosure; Page 192-194; 259pp; English.		
XX	The recombinant BPI (bacterial permeability-increasing), is designated		
CC	rBPI23. BPI peptides (AAR76244-458) were screened for bactericidal		
CC	effects on E. coli strains J5 and 011:B4 in a radial diffusion assay.		
CC	BPI peptides which retain antibacterial activity are expected to improve		
CC	the therapeutic effectiveness of antibiotics when concurrently		
CC	administered. Concurrent administration of BPI protein products and		
CC	antibiotics is shown to reverse resistance of a variety of gram-negative		
CC	organisms to antibiotics		
XX			
SQ	Sequence 487 AA;		
	Query Match	100.0%; Score 2507; DB 2; Length 487;	
	Best Local Similarity	100.0%; Pred. No. 4.3e-229;	
	Matches 487; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOGTAALQKEL	60
Db	1	MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPGVVVRISQKGLDYASQOGTAALQKEL	60
Qy	61	KRIKIPDYSDFKIKHLGKHYSFYSMDIREFQLPSSQISQSMVNPVGLKFSISNANIKISG	120
Db	61	KRIKIPDYSDFKIKHLGKHYSFYSMDIREFQLPSSQISQSMVNPVGLKFSISNANIKISG	120
Qy	121	KWKAQRFLKWSGNFDLSIEGMSISADLKLGSNFTSGKPTITCSCSHINSVHVHISKS	180
Db	121	KWKAQRFLKWSGNFDLSIEGMSISADLKLGSNFTSGKPTITCSCSHINSVHVHISKS	180
Qy	181	KVGWLIQLFHHKITESALRNKNSQCEKVTNSVSSKLPYFOTLPVMTKIDSVAGINYL	240
Db	181	KVGWLIQLFHHKITESALRNKNSQCEKVTNSVSSKLPYFOTLPVMTKIDSVAGINYL	240
Qy	241	VAPPATTATETLDVQMKGEFFSENHNHNPFPVMEFFPAADRMYVLGLSDYFFNTAGLV	300
Db	241	VAPPATTATETLDVQMKGEFFSENHNHNPFPVMEFFPAADRMYVLGLSDYFFNTAGLV	300
Qy	301	YQEAGVLKMTLRDDWIMPKESKFRITTKFPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360
Db	301	YQEAGVLKMTLRDDWIMPKESKFRITTKFPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ	360

Qy	361	PTGLTFYPAVDVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK	420
Db	361	PTGLTFYPAVDVQAFVLPNSLSLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK	420
Qy	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLGKGFPLTPARVQVLYNVVLPQHONFLLF	480
Db	421	HSNIGPFPVELLDIMNYIVPILVLPVNEKLGKGFPLTPARVQVLYNVVLPQHONFLLF	480
Qy	481	GADVYK 487	
Db	481	GADVYK 487	
	RESULT 14		
	AAW05852		
ID	AAW05852	standard; protein; 487 AA.	
XX	AAW05852;		
DT	25-MAR-2003	(revised)	
DT	18-DEC-1996	(first entry)	
XX	Recombinant bactericidal/permeability increasing protein.		
XX	Lipopolysaccharide binding protein; synergist; BPI; enhancement;		
KW	bactericidal/permeability increasing protein; potentiation; surgery;		
KW	Gram negative; bacterial infections; disinfection; sterilisation;		
KW	antibiotic; E.coli; polymorphonuclear leukocyte; mammalian.		
XX	Homo sapiens.		
OS			
XX			
PH	Key	Location/Qualifiers	
FT	Peptide	1. .31	
FT	/note= "signal peptide"		
FT	Protein	32. .487	
FT	/note= "mature recombinant BPI"		
XX	US5523288-A.		
PN	04-JUN-1996.		
PD	22-SEP-1994;	94US-00311611.	
XX	22-SEP-1993;	93US-00125651.	
PR	11-JUL-1994;	94US-00273401.	
XX	(XOMA ) XOMA CORP.		
XX	Little RG, Kung AHC, Cohen J, Lambert LH;		
XX	WPI; 1996-285780/29.		
DR	N-PSDB; AAT39396.		
XX	Compsn. for treating Gram negative bacterial infection - contg.		
PT	antibiotic and bactericidal-permeability increasing protein as synergist.		
XX	Disclosure; Col 163-168; 138pp; English.		
XX	This is the amino acid sequence of a bactericidal/permeability increasing		
CC	(BPI) protein. BPI is a protein isolated from the granules of mammalian		
CC	polymorphonuclear leukocytes. It is a 55 kD cationic protein which has		
CC	potent antibacterial activity against a broad range of Gram -ve bacteria.		
CC	The sequence was used to generate the peptides (AAW05853-W06074) which		
CC	were screened for bactericidal activity against E.coli strains J5 and		
CC	011:B4 in a radial diffusion assay. The BPI peptides can be used to		
CC	enhance the treatment of Gram -ve bacterial infections, prophylactically		
CC	for patients about to undergo surgery or for disinfection or		
CC	sterilisation. Administration of the BPI peptides together with an		
CC	antibiotic results in synergistic or potentiating bactericidal effects		
CC	greater than the effect of the individual peptide or antibiotic. Also the		
CC	BPI peptides can reverse the resistance of certain Gram -ve bacteria to		
CC	certain antibiotics e.g. carbenicillin, cefazolin. (Updated on 25-MAR-		



```

CC 2003 to correct PF field.)
XX
SQ Sequence 487 AA;

Query Match
Best Local Similarity 100.0%; Score 2507; DB 2; Length 487;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60
DB 1 MRENMGPCNAPRWVSLMVLVAIGTAVTAANPGVGVVIRISQKGLDYASQQTAAALQKEL 60
QY 61 KRIKIPDYSDFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
DB 61 KRIKIPDYSDFKIKHLGKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
QY 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
DB 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
QY 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYL 240
DB 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLOPYFOTLPVMTKIDSVAGINYL 240
QY 241 VAPPATTATLTDVQMKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGSLDYFFNTAGLV 300
DB 241 VAPPATTATLTDVQMKGEFYSENHNPPFPAPPVMEFPAADHDMVYLGSLDYFFNTAGLV 300
QY 301 YOEAGVLKMTLRDDMI PKESKFRLLTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
DB 301 YOEAGVLKMTLRDDMI PKESKFRLLTKPFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
QY 361 PTGLTFYPADVQAFAPVLPNSLASLFLIGMHTTGSMEVSASNSRLVGLKDLRLLELK 420
DB 361 PTGLTFYPADVQAFAPVLPNSLASLFLIGMHTTGSMEVSASNSRLVGLKDLRLLELK 420
QY 421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480
DB 421 HSNIGPPFVELLDIMNVIPIVLPRVNEKLOKGFPLPTPARVOLYNNVLOPHQNFLIF 480
QY 481 GADVYK 487
DB 481 GADVYK 487

RESULT 15
AAR97568
ID AAR97568 standard; protein; 487 AA.
AC AAR97568;
XX
XX 25-FEB-1997 (first entry)
DE Human bactericidal permeability increasing protein.
KW rBPI; recombinant; bactericidal permeability increasing protein;
KW anti-microbial; polyoxypropylene-polyoxyethylene block copolymer;
KW poloxamer; surfactant; inhibition; antibiotic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..31
XX /label= signal
XX Protein 32..487
XX /label= rBPI
XX
XX WO9621436-A1
XX
XX 18-JUL-1996.
XX
XX 16-JAN-1996; 96WO-US001095.
XX

```

Search completed: October 21, 2005, 11:26:46  
Job time : 174.559 secs

THIS PAGE BLANK (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:45 ; Search time 64.7154 Seconds  
(without alignments)  
1187.019 Million cell updates/sec

Title: US-10-629-516-2\_COPY\_10\_193  
Perfect score: 943  
Sequence: 1 CNAPRWSLMVLVAIGTAVT.....HVHISKVGNLQLFHKKI 184

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09D_PUBCOMB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19:	/cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
20:	/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21:	/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
22:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943	100.0	483	10	US-09-759-130B-408
2	943	100.0	483	13	US-10-042-431-38
3	943	100.0	483	16	US-10-741-790-408
4	943	100.0	483	16	US-10-473-127-1170
5	943	100.0	483	16	US-10-473-127-1170
6	943	100.0	487	9	US-09-765-527-265
7	943	100.0	487	9	US-09-760-397-16
8	943	100.0	487	9	US-09-881-490-206
9	943	100.0	487	9	US-09-942-021-2
10	943	100.0	487	9	US-09-733-613-2
11	943	100.0	487	9	US-09-728-938-2
					Sequence 408, App
					Sequence 38, Appl
					Sequence 408, App
					Sequence 1170, Ap
					Sequence 1241, Ap
					Sequence 265, App
					Sequence 16, Appl
					Sequence 206, App
					Sequence 2, Appl
					Sequence 2, Appl

12	943	100.0	487	9	US-09-782-642-2
13	943	100.0	487	9	US-09-255-245-2
14	943	100.0	487	9	US-09-941-198A-2
15	943	100.0	487	9	US-09-866-514-2
16	943	100.0	487	9	US-09-861-400-4
17	943	100.0	487	9	US-09-861-400-15
18	943	100.0	487	10	US-09-746-311-2
19	943	100.0	487	10	US-09-975-638B-3
20	943	100.0	487	10	US-09-416-828-2
21	943	100.0	487	10	US-09-480-234-2
22	943	100.0	487	13	US-10-006-557-2
23	943	100.0	487	14	US-10-226-810-2
24	943	100.0	487	14	US-10-128-139-2
25	943	100.0	487	14	US-10-196-460-2
26	943	100.0	487	14	US-10-146-136-2
27	943	100.0	487	14	US-10-209-621-28
28	943	100.0	487	14	US-10-131-686A-12
29	943	100.0	487	14	US-10-324-182-16
30	943	100.0	487	15	US-10-404-724-2
31	943	100.0	487	15	US-10-342-169A-2
32	943	100.0	487	15	US-10-299-985-2
33	943	100.0	487	15	US-10-162-743-2
34	943	100.0	487	15	US-10-446-628-69
35	943	100.0	487	15	US-10-446-628-146
36	943	100.0	487	15	US-10-319-786-69
37	943	100.0	487	15	US-10-359-013-13
38	943	100.0	487	16	US-10-716-389-2
39	943	100.0	487	16	US-10-473-127-1151
40	943	100.0	487	16	US-10-473-127-1152
41	943	100.0	487	16	US-10-473-127-1153
42	943	100.0	487	16	US-10-473-127-1154
43	943	100.0	487	16	US-10-473-127-1155
44	943	100.0	487	16	US-10-473-127-1156
45	943	100.0	487	16	US-10-473-127-1157

# ALIGNMENTS

RESULT 1  
US-09-759-130B-408  
; Sequence 408, Application US/09759130B  
; Publication No. US2003002279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirt, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: MP100-5350WNIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364

```

; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-759-1308-408

Query Match      100.0%; Score 943; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
    |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65

QY 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
    |||||
Db 66 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 125

QY 121 KMSGNFDLSIEGMSISADLKLGNSPTSGKPTTTCSSCSHNSVHVHISKSKVGLIQLF 180
    |||||
Db 126 KMSGNFDLSIEGMSISADLKLGNSPTSGKPTTTCSSCSHNSVHVHISKSKVGLIQLF 185

QY 181 HKKI 184
    |||||
Db 186 HKKI 189

RESULT 2
US-10-042-431-38
; Sequence 38, Application US/10042431
; Publication No. US20020182675A1
; GENERAL INFORMATION:
; APPLICANT: MCCARTHY, Sean A
; APPLICANT: BARNES, Thomas M
; APPLICANT: FRASER, Christopher C
; APPLICANT: SHARP, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 10147-6U2
; CURRENT APPLICATION NUMBER: US/10/042,431
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 38
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-042-431-38

Query Match      100.0%; Score 943; DB 13; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
    |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65

QY 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
    |||||

```

```

Db 66 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 125

QY 121 KMSGNFDLSIEGMSISADLKLGNSPTSGKPTTTCSSCSHNSVHVHISKSKVGLIQLF 180
    |||||
Db 126 KMSGNFDLSIEGMSISADLKLGNSPTSGKPTTTCSSCSHNSVHVHISKSKVGLIQLF 185

QY 181 HKKI 184
    |||||
Db 186 HKKI 189

RESULT 3
US-10-741-790-408
; Sequence 408, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: KIRST, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USES
; FILE REFERENCE: MPI00-5350NNIM
; CURRENT APPLICATION NUMBER: US/10/741,790
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 408
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-790-408

Query Match      100.0%; Score 943; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 3.4e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 60
    |||||
Db 6 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQOQTAALQKELKRIKIPDYS 65

QY 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
    |||||

```

Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 125  
Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 180  
Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 185  
Qy 181 HKKI 184  
Db 186 HKKI 189

RESULT 4

US-10-473-127-1170  
; Sequence 1170, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1170  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1170

Query Match 100.0%; Score 943; DB 16; Length 483;  
Best Local Similarity 100.0%; Pred. No. 3.4e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 60  
Db 6 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 65  
Qy 61 DSFKIKHLKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120  
Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 125  
Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 180  
Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 185  
Qy 181 HKKI 184  
Db 186 HKKI 189

RESULT 5

US-10-473-127-1241  
; Sequence 1241, Application US/10473127  
; Publication No. US20040236091A1  
; GENERAL INFORMATION:  
; APPLICANT: Zycos Inc.  
; TITLE OF INVENTION: TRANSLATIONAL PROFILING  
; FILE REFERENCE: 08191-026W01  
; CURRENT APPLICATION NUMBER: US/10/473,127  
; CURRENT FILING DATE: 2003-09-26  
; PRIOR APPLICATION NUMBER: 60/279,495

; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: 60/292,544  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/310,801  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/326,370  
; PRIOR FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: 60/336,780  
; PRIOR FILING DATE: 2001-12-04  
; PRIOR APPLICATION NUMBER: 60/358,985  
; PRIOR FILING DATE: 2002-02-20  
; NUMBER OF SEQ ID NOS: 2041  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1241  
; LENGTH: 483  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-473-127-1241

Query Match 100.0%; Score 943; DB 16; Length 483;  
Best Local Similarity 100.0%; Pred. No. 3.4e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 60  
Db 6 CNAPRWVSLMVLVAIGTAVTAANPVGVVVRSQKGLDYASOQGTAAQKELKRIKIPDYS 65  
Qy 61 DSFKIKHLKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 120  
Db 66 DSFKIKHLKGHYSFYSMDIREFQLPSSQISWPNVGLKFSISNANIKISGKWAQKRF 125  
Qy 121 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 180  
Db 126 KMSGNFDLSIEGMSISADLKLSNPTSGKPTTSCSSSHINSVHVHISKVGWLIQLF 185  
Qy 181 HKKI 184  
Db 186 HKKI 189

RESULT 6

US-09-765-527-265  
; Sequence 265, Application US/09765527  
; Patent No. US20020006638A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D.  
; TITLE OF INVENTION: Methods for Recombinant Microbial Production of  
Fusion Proteins and BPI-Derived Peptides  
; NUMBER OF SEQUENCES: 265  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshhall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/765,527  
; FILING DATE: 18-Jan-2001  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/621,803  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Borun, Michael F.  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/33199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 265:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-765-527-265

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189

Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 7  
US-09-760-397-16  
Sequence 16, Application US/09760397  
Patent No. US2002009781A1  
GENERAL INFORMATION:  
APPLICANT: Gavitt, Patrick D.  
APPLICANT: Better, Marc D.  
TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production  
FILE REFERENCE: 1103/11041US01  
CURRENT APPLICATION NUMBER: US/09/760,397  
CURRENT FILING DATE: 2001-01-12  
PRIOR APPLICATION NUMBER: 09/271,970  
PRIOR FILING DATE: 1999-03-18  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 16  
LENGTH: 487  
TYPE: PRT  
ORGANISM: Human  
US-09-760-397-16

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189

Qy 181 HKKI 184  
Db 190 HKKI 193

RESULT 8  
US-09-881-490-206  
Sequence 206, Application US/09881490  
Patent No. US20020077298A1  
GENERAL INFORMATION:  
APPLICANT: Little II, Roger G.  
Lim, Edward  
Fadem Mitchell B.  
TITLE OF INVENTION: Anti-Fungal Peptides  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th Floor Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/09/881,490  
FILING DATE: 14-Jun-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/119,858  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/372,105  
FILING DATE: 13-JAN-95  
APPLICATION NUMBER: 08/306,473  
FILING DATE: 15-SEP-94  
APPLICATION NUMBER: 08/273,540  
FILING DATE: 11-JUL-94  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-94  
APPLICATION NUMBER: 08/183,222  
APPLICATION NUMBER: 08/093,202  
FILING DATE: 15-JUL-93  
APPLICATION NUMBER: 08/030,644  
FILING DATE: 12-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 100-238/11021US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 206:  
US-09-881-490-206

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180

US-09-881-490-206

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180  
Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 189

Qy 181 HKKI 184  
Db 190 HKKI 193

US-09-881-490-206

Query Match 100.0%; Score 943; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 60  
Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVIRISQKGLDYASQOQGTAAALQKELKRIKIPDYS 69

Qy 61 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 120  
Db 70 DSPKIKHLGKHGHSFYSDMIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQKRF 129

Qy 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSSHINSVHVHISKSKVGLIQLF 180

Db 130 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 189  
 Qy 181 HKKI 184  
 Db 190 HKKI 193

RESULT 9  
 US-09-942-021-2  
 ; Sequence 2, Application US/09942021  
 ; Patent No. US2002009368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Little, Roger G. II  
 ; TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability  
 ; Increasing (BPI) Protein Products  
 ;  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
 ; STREET: 500 W. Madison Street, 34th Floor  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: USA  
 ; ZIP: 60661  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/942,021  
 ; FILING DATE: 27-Aug-2001  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/220,427  
 ; FILING DATE: 24-DEC-1998  
 ; APPLICATION NUMBER: 08/415,158  
 ; FILING DATE: March 31, 1995  
 ; APPLICATION NUMBER: 08/093,202  
 ; FILING DATE: July 15, 1993  
 ; APPLICATION NUMBER: 08/030,644  
 ; FILING DATE: March 12, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: McNicholas, Janet M.  
 ; REGISTRATION NUMBER: 32,918  
 ; REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/707-8889  
 ; TELEFAX: 312/707-9155  
 ; TELEX: <Unknown>  
 ;  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 487 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ;  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-942-021-2

Query Match 100.0%; Score 943; DB 9; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CNAPRWVSLMLVLAIGTAVTAAPVGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
 Db 10 CNAPRWVSLMLVLAIGTAVTAAPVGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69  
 Qy 61 DSFKIKHLKGHYFVSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRL 120  
 Db 70 DSFKIKHLKGHYFVSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRL 129  
 Qy 121 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 180  
 Db 130 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 189

Db 130 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 189  
 Qy 181 HKKI 184  
 Db 190 HKKI 193

RESULT 10  
 US-09-733-613-2  
 ; Sequence 2, Application US/09733613  
 ; Patent No. US20020094952A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Friedmann, Nadav  
 ; Scannon, Patrick J.  
 ; van Deventer, Sander J.H.  
 ; von der Mohlen, Marijke A.M.  
 ; Wedel, Nancy  
 ;  
 ; TITLE OF INVENTION: Human Therapeutic Uses of BPI Protein Products  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive  
 ; CITY: Chicago  
 ; STATE: Illinois  
 ; COUNTRY: United States of America  
 ; ZIP: 60606-6402  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ;  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/733,613  
 ; FILING DATE: 08-Dec-2000  
 ; CLASSIFICATION: <Unknown>  
 ;  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/388,758  
 ; FILING DATE: 1999-09-02  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Michael F. Borun  
 ; REGISTRATION NUMBER: 25,447  
 ; REFERENCE/DOCKET NUMBER: 27129/32451  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 312/474-6300  
 ; TELEFAX: 312/474-0448  
 ; TELEX: 25-3856  
 ;  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 487 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ;  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-733-613-2

Query Match 100.0%; Score 943; DB 9; Length 487;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-84;  
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CNAPRWVSLMLVLAIGTAVTAAPVGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 60  
 Db 10 CNAPRWVSLMLVLAIGTAVTAAPVGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYS 69  
 Qy 61 DSFKIKHLKGHYFVSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRL 120  
 Db 70 DSFKIKHLKGHYFVSMDIREFQLPSSQISWVPNVGLKFSISNANIKISGKWKAKQKRL 129  
 Qy 121 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 180  
 Db 130 KMSGNFSLIEGMSISADLKLGSNPTSGKPTTICSSSHINSVHVHISKVGVWLIQLF 189

Db 190 HKKI 193

RESULT 11

US-09-728-938-2

; Sequence 2, Application US/09728938

; Patent No. US20020103114A1

; GENERAL INFORMATION:

; APPLICANT: Giroir, Brett P.

; TITLE OF INVENTION: Therapeutic Uses of BPI Protein Products

; for Human Meningococemia

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/728,938

; FILING DATE: 30-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/365,858

; FILING DATE: <Unknown>

; APPLICATION NUMBER: 08/927,437

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Sharp, Jeffrey S.

; REGISTRATION NUMBER: 31,879

; REFERENCE/DOCKET NUMBER: 27129/33248

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 487 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-728-938-2

Query Match 100.0%; Score 943; DB 9; Length 487;

Best Local Similarity 100.0%; Pred. No. 3.5e-84;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60

Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 69

QY 61 DSPKIKHLGKHGHSFYFSDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQRFL 120

Db 70 DSPKIKHLGKHGHSFYFSDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQRFL 129

QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHNSVHVHISKSVGWLILQLF 180

Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHNSVHVHISKSVGWLILQLF 189

QY 181 HKKI 184

Db 190 HKKI 193

RESULT 12

US-09-782-642-2

; Sequence 2, Application US/09782642

; Patent No. US20020103118A1

; GENERAL INFORMATION:

; APPLICANT: Lewis H. Lambert, Jr.

; TITLE OF INVENTION: Treatment of Mycobacterial Diseases

; by Administration of

; Bactericidal/Permeability-Increasing

; Protein Product

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/782,642

; FILING DATE: 13-Feb-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/626,646

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 31293

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

; TELEX: 25-3856

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 487 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-782-642-2

Query Match 100.0%; Score 943; DB 9; Length 487;

Best Local Similarity 100.0%; Pred. No. 3.5e-84;

Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 60

Db 10 CNAPRWVSLMVLVAIGTAVTAANPGVVVRISQKGLDYASQQTAAALQKELKRIKIPDYS 69

QY 61 DSPKIKHLGKHGHSFYFSDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQRFL 120

Db 70 DSPKIKHLGKHGHSFYFSDIREFQLPSSQISWPNVGLKFSISNANIKISGKWKAKQRFL 129

QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHNSVHVHISKSVGWLILQLF 180

Db 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTTICSSCSSHNSVHVHISKSVGWLILQLF 189

QY 181 HKKI 184

Db 190 HKKI 193

RESULT 13

US-09-255-245-2

; Sequence 2, Application US/09255245

; Patent No. US20020119918A1

; GENERAL INFORMATION:



```

; APPLICANT: Cartoll, Stephen F.
; TITLE OF INVENTION: THERAPEUTIC USES OF N-TERMINAL BPI PROTEIN
; TITLE OF INVENTION: PRODUCTS IN ANCA-POSITIVE PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,245
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/742,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/33565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-255-245-2

Query Match 100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANVPVGVVVRISQKGLDYASQOGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWVSLMVLVAIGTAVTAANVPVGVVVRISQKGLDYASQOGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
DB 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLF 180
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 14
US-09-941-198A-2
; Sequence 2, Application US/09941198A
; Patent No. US2002012819A1
; GENERAL INFORMATION:
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: METHODS OF TREATING CONDITIONS
; ASSOCIATED WITH CORNEAL INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun

```

```

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,198A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/557,289
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-941-198A-2

Query Match 100.0%; Score 943; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 3.5e-84;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNAPRWVSLMVLVAIGTAVTAANVPVGVVVRISQKGLDYASQOGTAAALQKELKRIKIPDYS 60
DB 10 CNAPRWVSLMVLVAIGTAVTAANVPVGVVVRISQKGLDYASQOGTAAALQKELKRIKIPDYS 69
QY 61 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 120
DB 70 DSFKIKHLGKHGHSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISGKWKAKRFL 129
QY 121 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLF 180
DB 130 KMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSSSHINSVHVHISKSKVGLIQLF 189
QY 181 HKKI 184
DB 190 HKKI 193

RESULT 15
US-09-866-514-2
; Sequence 2, Application US/09866514
; Patent No. US20020137050A1
; GENERAL INFORMATION:
; APPLICANT: Elsbach and Weiss
; TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING
; PROTEIN FRAGMENTS
; FILE REFERENCE: 28297/32248B
; CURRENT APPLICATION NUMBER: US/09/866,514
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/309,217
; PRIOR FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT

```

; ORGANISM: Homo sapiens  
US-09-866-514-2

Query Match	100.0%	Score 943;	DB 9;	Length 487;
Best Local Similarity	100.0%;	Pred. No. 3.5e-84;		
Matches 184;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CNAPRWLSLMLVLAIGTAVTAANVPGVVVRIISQKGLDYASQQGTAALQKELKRIKIKIPDYS	60	
Db	10	CNAPRWLSLMLVLAIGTAVTAANVPGVVVRIISQKGLDYASQQGTAALQKELKRIKIKIPDYS	69	
Qy	61	DSFKIKHLKGHYSFYSNDIREFOLPSSQISMPNVNGLKFSISNANIKISGKWKAAQKRFL	120	
Db	70	DSFKIKHLKGHYSFYSNDIREFOLPSSQISMPNVNGLKFSISNANIKISGKWKAAQKRFL	129	
Qy	121	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF	180	
Db	130	KMSGNFDLSIEGMSISADLKLGNPTSGKPTITCSCSSHINSVHVHISKSKVGLIQLF	189	
Qy	181	HKKI	184	
Db	190	HKKI	193	

Search completed: October 21, 2005, 11:37:02  
Job time : 65.7154 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2005, 11:22:45 ; Search time 171.285 Seconds  
(without alignments)  
1187.019 Million cell updates/sec

Title: US-10-629-516-2

Perfect score: 2507

Sequence: 1 MRENARGPCNAPRWVSLMV.....NVVLQHQNFLFGADVVK 487

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1862951 seqs, 417491010 residues

Total number of hits satisfying chosen parameters: 1862951

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PTCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2507	100.0	487	9	US-09-765-527-265
2	2507	100.0	487	9	US-09-760-397-16
3	2507	100.0	487	9	US-09-881-490-206
4	2507	100.0	487	9	US-09-942-021-2
5	2507	100.0	487	9	US-09-733-613-2
6	2507	100.0	487	9	US-09-728-938-2
7	2507	100.0	487	9	US-09-782-642-2
8	2507	100.0	487	9	US-09-255-245-2
9	2507	100.0	487	9	US-09-941-198A-2
10	2507	100.0	487	9	US-09-866-514-2
11	2507	100.0	487	9	US-09-861-400-15

12	2507	100.0	487	10	US-09-746-311-2	Sequence 2, Appli
13	2507	100.0	487	10	US-09-975-638B-3	Sequence 3, Appli
14	2507	100.0	487	10	US-09-416-828-2	Sequence 2, Appli
15	2507	100.0	487	10	US-09-480-234-2	Sequence 2, Appli
16	2507	100.0	487	13	US-10-006-557-2	Sequence 2, Appli
17	2507	100.0	487	14	US-10-226-810-2	Sequence 2, Appli
18	2507	100.0	487	14	US-10-128-139-2	Sequence 2, Appli
19	2507	100.0	487	14	US-10-196-460-2	Sequence 2, Appli
20	2507	100.0	487	14	US-10-146-136-2	Sequence 2, Appli
21	2507	100.0	487	14	US-10-209-621-28	Sequence 28, Appli
22	2507	100.0	487	14	US-10-131-686A-12	Sequence 12, Appli
23	2507	100.0	487	14	US-10-324-182-16	Sequence 16, Appli
24	2507	100.0	487	15	US-10-404-724-2	Sequence 2, Appli
25	2507	100.0	487	15	US-10-342-169A-2	Sequence 2, Appli
26	2507	100.0	487	15	US-10-299-985-2	Sequence 2, Appli
27	2507	100.0	487	15	US-10-162-743-2	Sequence 69, Appli
28	2507	100.0	487	15	US-10-446-628-69	Sequence 146, App
29	2507	100.0	487	15	US-10-446-628-146	Sequence 69, Appli
30	2507	100.0	487	15	US-10-319-786-69	Sequence 13, Appli
31	2507	100.0	487	16	US-10-359-013-13	Sequence 2, Appli
32	2507	100.0	487	16	US-10-716-389-2	Sequence 1151, Ap
33	2507	100.0	487	16	US-10-473-127-1151	Sequence 1152, Ap
34	2507	100.0	487	16	US-10-473-127-1152	Sequence 1153, Ap
35	2507	100.0	487	16	US-10-473-127-1153	Sequence 1154, Ap
36	2507	100.0	487	16	US-10-473-127-1154	Sequence 1155, Ap
37	2507	100.0	487	16	US-10-473-127-1155	Sequence 1156, Ap
38	2507	100.0	487	16	US-10-473-127-1156	Sequence 1157, Ap
39	2507	100.0	487	16	US-10-473-127-1157	Sequence 1158, Ap
40	2507	100.0	487	16	US-10-473-127-1158	Sequence 1159, Ap
41	2507	100.0	487	16	US-10-473-127-1159	Sequence 1160, Ap
42	2507	100.0	487	16	US-10-473-127-1160	Sequence 1161, Ap
43	2507	100.0	487	16	US-10-473-127-1161	Sequence 1162, Ap
44	2507	100.0	487	16	US-10-473-127-1162	Sequence 1163, Ap
45	2507	100.0	487	16	US-10-473-127-1163	

## ALIGNMENTS

### RESULT 1

US-09-765-527-265

; Sequence 265, Application US/09765527

; Patent No. US20020006638A1

; GENERAL INFORMATION:

; APPLICANT: Better, Marc D.

; TITLE OF INVENTION: Methods for Recombinant Microbial Production of

; FUSION PROTEINS AND BPI-DERIVED PEPTIDES

; NUMBER OF SEQUENCES: 265

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/765,527

; FILING DATE: 18-Jan-2001

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/621,803

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Borun, Michael F.

; REGISTRATION NUMBER: 25,447

; REFERENCE/DOCKET NUMBER: 27129/33199

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312/474-6300

; TELEFAX: 312/474-0448

```
;
;
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 487 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-765-527-265

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKEL 60
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
Qy 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNHPPPPAPPVMEFPAAHDMRVYLGSLDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNHPPPPAPPVMEFPAAHDMRVYLGSLDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTTPAVDVQAFVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTTPAVDVQAFVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHONFLFF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHONFLFF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 3
US-09-881-490-206
; Sequence 206, Application US/09881490
; Patent No. US2002007298A1
; GENERAL INFORMATION:
; APPLICANT: Little II, Roger G.
; Lim, Edward
; Fadem, Mitchell B.
; TITLE OF INVENTION: Anti-Fungal Peptides
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th Floor Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/881,490
; APPLICATION NUMBER: 09/119,858
; FILING DATE: 14-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/119,858
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/372,105
; FILING DATE: 13-JAN-95
; APPLICATION NUMBER: 08/306,473
; FILING DATE: 15-SEP-94
; APPLICATION NUMBER: 08/273,540

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASQOQTAALQKEL 60
Qy 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKHGHSFYSDIREFQLPSSQISWPNVGLKFSISNANIKISG 120
Qy 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSSKLQPYFQTLPMVTKIDSVAGINYL 240
Qy 241 VAPPATTAETLDVQMKGEFYSENHNHPPPPAPPVMEFPAAHDMRVYLGSLDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNHPPPPAPPVMEFPAAHDMRVYLGSLDYFFNTAGLV 300
Qy 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNNMKIQIHVSASTPPHLSVQ 360
Qy 361 PTGLTTPAVDVQAFVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Db 361 PTGLTTPAVDVQAFVLPNSLSASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELK 420
Qy 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHONFLFF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVPRVNEKLGKGFPLTPARVOLYNVVLQPHONFLFF 480
Qy 481 GADVYK 487
Db 481 GADVYK 487

RESULT 2
US-09-760-397-16
; Sequence 16, Application US/09760397
; Patent No. US20020009781A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Gavitt, Patrick D.
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production
; FILE REFERENCE: 1103/11041US01
; CURRENT APPLICATION NUMBER: US/09/760,397
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/271,970
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
; US-09-760-397-16

Query Match      100.0%; Score 2507; DB 9; Length 487;
```

Fri Oct 21 12:25:52 2005

FILING DATE: 11-JUL-94  
APPLICATION NUMBER: 08/209,762  
FILING DATE: 11-MAR-94  
APPLICATION NUMBER: 08/183,222  
FILING DATE: 14-JAN-94  
APPLICATION NUMBER: 08/093,202  
FILING DATE: 15-JUL-93  
APPLICATION NUMBER: 08/030,644  
FILING DATE: 12-MAR-93  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 100-238/11021US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248

INFORMATION FOR SEQ ID NO: 206:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 206:

US-09-881-490-206

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Mismatches 0; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQTAAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQTAAALQKEL 60  
QY 61 KRIKIPDYSDFSKIKHLKGHYSFYMDIREFQPSQISQVNPVGLKFSINANIKISG 120  
DB 61 KRIKIPDYSDFSKIKHLKGHYSFYMDIREFQPSQISQVNPVGLKFSINANIKISG 120  
QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKSGNPTSGKPTITCSCSSHINSVHVHISKS 180  
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKSGNPTSGKPTITCSCSSHINSVHVHISKS 180  
QY 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSKLQPYFQTLPMVKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSKLQPYFQTLPMVKIDS VAGINYL 240  
QY 241 VAPPATTATLTVQMKGEFYSENHNPPFPVMEFFAAHDMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTATLTVQMKGEFYSENHNPPFPVMEFFAAHDMVYLGSLDYFFNTAGLV 300  
QY 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQFAVLPNSIASLFLIGMTTGSMEVSAESNRLVGLKLDRLLELK 420  
DB 361 PTGLTFYPADVQFAVLPNSIASLFLIGMTTGSMEVSAESNRLVGLKLDRLLELK 420  
QY 421 HSNIGFPVELLDQIMNYIVPILVLPVNEKIQKGFPLTPARVQLYNNVLOPHONFLIF 480  
DB 421 HSNIGFPVELLDQIMNYIVPILVLPVNEKIQKGFPLTPARVQLYNNVLOPHONFLIF 480  
QY 481 GADVYK 487  
DB 481 GADVYK 487

RESULT 4

US-09-942-021-2

Sequence 2, Application US/09942021  
Patent No. US20020090368A1  
GENERAL INFORMATION:  
APPLICANT: Little, Roger G. II

TITLE OF INVENTION: Therapeutic Uses of Bactericidal/Permeability  
Increasing (BPI) Protein Products

NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Hald & Malloy, Ltd.  
STREET: 500 W. Madison Street, 34th Floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/942,021  
FILING DATE: 27-Aug-2001  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/220,427  
FILING DATE: 24-DEC-1998  
APPLICATION NUMBER: 08/415,158  
FILING DATE: March 31, 1995  
APPLICATION NUMBER: 08/093,202  
FILING DATE: July 15, 1993  
APPLICATION NUMBER: 08/030,644  
FILING DATE: March 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 11004US07 / 100-224.P1.C3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 487 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-942-021-2

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209; Mismatches 0; Indels 0; Gaps 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQTAAALQKEL 60  
DB 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAAVNPVGVVRIISQKGLDYASQQTAAALQKEL 60  
QY 61 KRIKIPDYSDFSKIKHLKGHYSFYMDIREFQPSQISQVNPVGLKFSINANIKISG 120  
DB 61 KRIKIPDYSDFSKIKHLKGHYSFYMDIREFQPSQISQVNPVGLKFSINANIKISG 120  
QY 121 KWAQKRFKMGSGNFDLSIEGMSISADLKSGNPTSGKPTITCSCSSHINSVHVHISKS 180  
DB 121 KWAQKRFKMGSGNFDLSIEGMSISADLKSGNPTSGKPTITCSCSSHINSVHVHISKS 180  
QY 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSKLQPYFQTLPMVKIDS VAGINYL 240  
DB 181 KVGWLIQLFHKKIESALRNKMSQCEKVTNSVSKLQPYFQTLPMVKIDS VAGINYL 240  
QY 241 VAPPATTATLTVQMKGEFYSENHNPPFPVMEFFAAHDMVYLGSLDYFFNTAGLV 300  
DB 241 VAPPATTATLTVQMKGEFYSENHNPPFPVMEFFAAHDMVYLGSLDYFFNTAGLV 300  
QY 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360  
DB 301 YQEAGVLKMTLRDDMI PKESKRLTTKFGTFLPEVAKKFPNNKIQIHVSASTPPHLSVQ 360

QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420  
QY 421 HSNIGPPVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVLOPHQNFLLF 480  
DB 421 HSNIGPPVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVLOPHQNFLLF 480  
QY 481 GADVVK 487  
DB 481 GADVVK 487  
RESULT 5  
US-09-733-613-2  
; Sequence 2, Application US/09733613  
; Patent No. US20020094952A1  
; GENERAL INFORMATION:  
; APPLICANT: Friedmann, Nadav  
; Scannon, Patrick J.  
; van Deventer, Sander J.H.  
; von der Mohlen, Marijke A.M.  
; Wedel, Nancy  
; TITLE OF INVENTION: Human Therapeutic Uses of BPI Protein Products  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/733.613  
; FILING DATE: 08-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/388,758  
; FILING DATE: 1993-09-02  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Michael F. Borun  
; REGISTRATION NUMBER: 25,447  
; REFERENCE/DOCKET NUMBER: 27129/32451  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-733-613-2  
Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MRENWAGPCNAPRWVSLWLVALGTAVTAAVNPGVVVRISQKGLDYASQOGTAALQKEL 60  
DB 1 MRENWAGPCNAPRWVSLWLVALGTAVTAAVNPGVVVRISQKGLDYASQOGTAALQKEL 60  
QY 61 KRKIPDYSDFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120  
DB 61 KRKIPDYSDFKIKHLKGHYSPYMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

QY 121 KWKAQRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHNSVHVHISKS 180  
DB 121 KWKAQRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHNSVHVHISKS 180  
QY 181 KYGWLIIQPHKIESALRNKMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYGL 240  
DB 181 KYGWLIIQPHKIESALRNKMSQVCEKVTNSVSSKLQPYFOTLPVMTKIDSVAGINYGL 240  
QY 241 VAPPATTAAETLDVQMKGEFYSNNHNPFPFAPPVMEFFPAADHDMVYLGLSDYFFENTAGLV 300  
DB 241 VAPPATTAAETLDVQMKGEFYSNNHNPFPFAPPVMEFFPAADHDMVYLGLSDYFFENTAGLV 300  
QY 301 YQAGVLMKTLRDDMIKPESKFERLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
DB 301 YQAGVLMKTLRDDMIKPESKFERLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
QY 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420  
DB 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGBELKDLRLLELK 420  
QY 421 HSNIGPPVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVLOPHQNFLLF 480  
DB 421 HSNIGPPVELLDQIMNYIVPILVPRVNEKLOKGFPLPTPARVQLYNVVLOPHQNFLLF 480  
QY 481 GADVVK 487  
DB 481 GADVVK 487  
RESULT 6  
US-09-728-938-2  
; Sequence 2, Application US/09728938  
; Patent No. US20020103114A1  
; GENERAL INFORMATION:  
; APPLICANT: Giroir, Brett P.  
; Scannon, Patrick J.  
; TITLE OF INVENTION: Therapeutic Uses of BPI Protein Products  
; for Human Meningococemia  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/728,938  
; FILING DATE: 30-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/365,858  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: 08/927,437  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sharp, Jeffrey S.  
; REGISTRATION NUMBER: 31,879  
; REFERENCE/DOCKET NUMBER: 27129/33248  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 487 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

```
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-728-938-2

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKEL 60

Qy 61 KRIKIPDYSDSFKIKHLKGHYSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDSFKIKHLKGHYSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTATETLDVQMGKGFYSENHNPPPPFAPPVMEFPAADRMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTATETLDVQMGKGFYSENHNPPPPFAPPVMEFPAADRMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTLPVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTLPVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPFFVELLDIMNVIPIVLPVPRVNEKIQGFPLTPARVOLYNVVLQPHONFLLF 480
Db 421 HSNIGPFFVELLDIMNVIPIVLPVPRVNEKIQGFPLTPARVOLYNVVLQPHONFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 7
US-09-782-642-2
; Sequence 2, Application US/09782642
; Patent No. US20020103118A1
; GENERAL INFORMATION:
; APPLICANT: Lewis H. Lambert, Jr.
; TITLE OF INVENTION: Treatment of Mycobacterial Diseases
; by Administration of
; Bactericidal/Permeability-Increasing
; Protein Product
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/782,642
; APPLICATION NUMBER: US/09/782,642
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,646
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael F.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 31293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-642-2

Query Match      100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPGVVRISQKGLDYASQOQGTAAALQKEL 60

Qy 61 KRIKIPDYSDSFKIKHLKGHYSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDSFKIKHLKGHYSFYSDIRFQLPSSQISMVNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKNSQVCEKVTNSVSSKLOPYQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPATTATETLDVQMGKGFYSENHNPPPPFAPPVMEFPAADRMVYLGSDYFFNTAGLV 300
Db 241 VAPPATTATETLDVQMGKGFYSENHNPPPPFAPPVMEFPAADRMVYLGSDYFFNTAGLV 300

Qy 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTLPVAKKFNMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKWTLRDDMI PKESKFRLLTKPGFTLPVAKKFNMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPFFVELLDIMNVIPIVLPVPRVNEKIQGFPLTPARVOLYNVVLQPHONFLLF 480
Db 421 HSNIGPFFVELLDIMNVIPIVLPVPRVNEKIQGFPLTPARVOLYNVVLQPHONFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 8
US-09-255-245-2
; Sequence 2, Application US/09255245
; Patent No. US20020119918A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Stephen F.
; TITLE OF INVENTION: THERAPEUTIC USES OF N-TERMINAL BPI PROTEIN
; PRODUCTS IN ANCA-POSITIVE PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
```

```

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/255,245
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/742,985
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/33565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-255-245-2

```

```

Query Match 100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASOOGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASOOGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSDYFNTAGLV 300
Db 241 VAPPTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSDYFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPLSVQ 360

Qy 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEIKLDRLLLELK 420
Db 361 PTGLTTFYPAVDVQAFVLPNSSLASFLIGHMTTGSMEVSAESNRLVGEIKLDRLLLELK 420

Qy 421 HSNIGPFPVELLDQIMNVIVILVLPVNEKIQKGFPLTPARVOLNVVILQPHQNFLLF 480
Db 421 HSNIGPFPVELLDQIMNVIVILVLPVNEKIQKGFPLTPARVOLNVVILQPHQNFLLF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

```

```

RESULT 9
US-09-941-198A-2
; Sequence 2, Application US/09941198A
; Patent No. US20020128191A1
; GENERAL INFORMATION:
; APPLICANT: Scannon, Patrick J.
; TITLE OF INVENTION: METHODS OF TREATING CONDITIONS ASSOCIATED WITH CORNEAL INJURY
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/941,198A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/557,289
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Borun, Michael P.
; REGISTRATION NUMBER: 25,447
; REFERENCE/DOCKET NUMBER: 27129/33006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-941-198A-2

```

```

Query Match 100.0%; Score 2507; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASOOGTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANVPGVVVRISQKGLDYASOOGTAALQKEL 60

Qy 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120
Db 61 KRKIPDYSDFKIKHLGKGHYSFYSDMDIREFQLPSSQISMVNPVGLKFSISNANIKISG 120

Qy 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180
Db 121 KWKAKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180

Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLQPYFQTLPVMTKIDSVAGINYL 240

Qy 241 VAPPTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSDYFNTAGLV 300
Db 241 VAPPTAETLDVQMKGEFYSENHNPPPPAPPVMEFPAAHDMRVYLGSDYFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRITTKFPGFTFLPEVAKKFPNMKI QIHVSASTPPLSVQ 360

```



Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLEVAKKFPNMKIQIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 10  
US-09-866-514-2  
; Sequence 2, Application US/09866514  
; Patent No. US20020137050A1  
; GENERAL INFORMATION:  
; APPLICANT: Elsbach and Weiss  
; TITLE OF INVENTION: THERAPEUTIC USES OF BACTERICIDAL/PERMEABILITY-INCREASING  
; TITLE OF INVENTION: PROTEIN FRAGMENTS  
; FILE REFERENCE: 28297/32248B  
; CURRENT APPLICATION NUMBER: US/09/866,514  
; CURRENT FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 09/309,217  
; PRIOR FILING DATE: 1999-05-10  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-866-514-2

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQGLDYASQGTAAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQGLDYASQGTAAALQKEL 60  
Qy 61 KRIKIPYSDSFKIKHLKGHSYFSYMDIRBQFQPSQISMVPNVGLKFSISNANIKISG 120  
Db 61 KRIKIPYSDSFKIKHLKGHSYFSYMDIRBQFQPSQISMVPNVGLKFSISNANIKISG 120  
Qy 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
Db 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDSAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDSAGINYL 240  
Qy 241 VAPPATTATLTVQMKGFYSENHNPPFPVMEFPAADHDMVYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTATLTVQMKGFYSENHNPPFPVMEFPAADHDMVYLGLSDYFFNTAGLV 300  
Qy 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLEVAKKFPNMKI QIHVSASTPPHLSVQ 360  
Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLEVAKKFPNMKI QIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487

Db 481 GADVYK 487

RESULT 11  
US-09-861-400-15  
; Sequence 15, Application US/09861400  
; Patent No. US20020146761A1  
; GENERAL INFORMATION:  
; APPLICANT: Scott, Randal W  
; APPLICANT: Marra, Marian N  
; TITLE OF INVENTION: RECOMBINANT ENDOTOXIN-NEUTRALIZING PROTEINS  
; FILE REFERENCE: 1103/11307US01  
; CURRENT APPLICATION NUMBER: US/09/861,400  
; CURRENT FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: 08/431,517  
; PRIOR FILING DATE: 1995-05-01  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: human  
; FEATURE:  
; OTHER INFORMATION: human BPI amino acid (Figure 5)  
; NAME/KEY: SIGNAL  
; LOCATION: (1)..(31)  
; NAME/KEY: CHAIN  
; LOCATION: (32)..(487)  
US-09-861-400-15

Query Match 100.0%; Score 2507; DB 9; Length 487;  
Best Local Similarity 100.0%; Pred. No. 1.7e-209;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQGLDYASQGTAAALQKEL 60  
Db 1 MRENARGPCNAPRWVSLMVLVAICTAVTAANPGVVVRI SQGLDYASQGTAAALQKEL 60  
Qy 61 KRIKIPYSDSFKIKHLKGHSYFSYMDIRBQFQPSQISMVPNVGLKFSISNANIKISG 120  
Db 61 KRIKIPYSDSFKIKHLKGHSYFSYMDIRBQFQPSQISMVPNVGLKFSISNANIKISG 120  
Qy 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
Db 121 KWKAKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSCSSHINSVHVHISKS 180  
Qy 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDSAGINYL 240  
Db 181 KVGWLIQLFHKKIESALRNKMSQVCEKVTNSVSKLOPYFQTLPMVTKIDSAGINYL 240  
Qy 241 VAPPATTATLTVQMKGFYSENHNPPFPVMEFPAADHDMVYLGLSDYFFNTAGLV 300  
Db 241 VAPPATTATLTVQMKGFYSENHNPPFPVMEFPAADHDMVYLGLSDYFFNTAGLV 300  
Qy 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLEVAKKFPNMKI QIHVSASTPPHLSVQ 360  
Db 301 YQAGVLKQTLRDDMI PKESKRLTTKFFGTFLEVAKKFPNMKI QIHVSASTPPHLSVQ 360  
Qy 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Db 361 PTGLTFYPAVDVQAFAPVLPNSLASLFLIGHMHTTGSMEVSAESNRLVGELKLDRLLELK 420  
Qy 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Db 421 HSNIGPPFVELLDQIMNVIIPILVLPVNEKLOKGFPLTPARVOLYNNVLOPHQNFLLF 480  
Qy 481 GADVYK 487  
Db 481 GADVYK 487

RESULT 12

```
US-09-746-311-2
; Sequence 2, Application US/09746311
; Publication No. US20030017143A1
; GENERAL INFORMATION:
; APPLICANT: Little, II, Roger G.
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING
; TITLE OF INVENTION: METABOLIC OXIDATION-REDUCTION INDICATOR DYES
; FILE REFERENCE: 27129/36226
; CURRENT APPLICATION NUMBER: US/09/746,311
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/143,290
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-311-2

Query Match      100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Db      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Qy      61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISMVNVNGLKFSISNANIKISG 120
Db      61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISMVNVNGLKFSISNANIKISG 120
Qy      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCCSSSHINSVHVHISKS 180
Db      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCCSSSHINSVHVHISKS 180
Qy      181 KVGWLIQLFHKKIESALRNKWNQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Db      181 KVGWLIQLFHKKIESALRNKWNQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Qy      241 VAPPATTAETLDVQMGGEFYSENHNPPFPAPPVMEFFPAAHDMRVYLGLSDYFFNTAGLV 300
Db      241 VAPPATTAETLDVQMGGEFYSENHNPPFPAPPVMEFFPAAHDMRVYLGLSDYFFNTAGLV 300
Qy      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Qy      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Qy      421 HSNIGPFPVELLDIMNVIYVILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Db      421 HSNIGPFPVELLDIMNVIYVILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Qy      481 GADVYK 487
Db      481 GADVYK 487

RESULT 13
US-09-746-311-2
; Sequence 3, Application US/09975638B
; Publication No. US20030166528A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Jong Jye
; TITLE OF INVENTION: Antifungal Compound
; FILE REFERENCE: 27129/37753
; CURRENT APPLICATION NUMBER: US/09/975,638B
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: 60/239,709
; PRIOR FILING DATE: 2000-10-11

US-09-746-311-2
; Sequence 2, Application US/09746311
; Publication No. US20030017143A1
; GENERAL INFORMATION:
; APPLICANT: Little, II, Roger G.
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL ANTIMICROBIAL AGENTS USING
; TITLE OF INVENTION: METABOLIC OXIDATION-REDUCTION INDICATOR DYES
; FILE REFERENCE: 27129/36226
; CURRENT APPLICATION NUMBER: US/09/746,311
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/143,290
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-638B-3

Query Match      100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Db      1 MRENARGPCNAPRWVSLMVLVAIGTAVTAANPVGVVVRIISQKGLDYASQOQTAALQKEL 60
Qy      61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISMVNVNGLKFSISNANIKISG 120
Db      61 KRKIPDYSDFKIKHLGKGHYFSYMDIREFOLPSSQISMVNVNGLKFSISNANIKISG 120
Qy      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCCSSSHINSVHVHISKS 180
Db      121 KWKAQKRFKLMKSGNFDLSIEGMSISADLKLGSNPTSGKPTITCCSSSHINSVHVHISKS 180
Qy      181 KVGWLIQLFHKKIESALRNKWNQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Db      181 KVGWLIQLFHKKIESALRNKWNQVCEKVTNSVSSKLQPYFQTLPVMTKIDSVAGINYL 240
Qy      241 VAPPATTAETLDVQMGGEFYSENHNPPFPAPPVMEFFPAAHDMRVYLGLSDYFFNTAGLV 300
Db      241 VAPPATTAETLDVQMGGEFYSENHNPPFPAPPVMEFFPAAHDMRVYLGLSDYFFNTAGLV 300
Qy      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Db      301 YQEAGVLKMTLRDDMIPEKSKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQ 360
Qy      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db      361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Qy      421 HSNIGPFPVELLDIMNVIYVILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Db      421 HSNIGPFPVELLDIMNVIYVILVLRVNEKLOKGFPLPTPARVQLYNNVVLQPHQNFLLF 480
Qy      481 GADVYK 487
Db      481 GADVYK 487

RESULT 14
US-09-416-828-2
; Sequence 2, Application US/09416828
; Publication No. US20030171265A1
; GENERAL INFORMATION:
; APPLICANT: Ammons, William Steve et al.
; TITLE OF INVENTION: Method of Treating Conditions Associated with
; TITLE OF INVENTION: Intestinal Ischemia/Reperfusion
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,828
; FILING DATE:
```

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/756,164
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharp, Jeffrey S.
; REGISTRATION NUMBER: 31,879
; REFERENCE/DOCKET NUMBER: 27129/32043
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-416-828-2

Query Match 100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAAVNPGVVVRIISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAAVNPGVVVRIISQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHYSFYSMDIRFQLPSSQISWPNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSFYSMDIRFQLPSSQISWPNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPYFQTLPMVTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFFAAHDMVYGLSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFFAAHDMVYGLSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVLPVNEKLOKGFPLPTPARVOLYNVVLQPHONFLIF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVLPVNEKLOKGFPLPTPARVOLYNVVLQPHONFLIF 480

Qy 481 GADVVYK 487
Db 481 GADVVYK 487

RESULT 15
US-09-480-234-2
; Sequence 2, Application US/09480234
; Publication No. US20030194377A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Stephen F.
; Scannon, Patrick J.
; Gavit, Patrick D.
; TITLE OF INVENTION: IMPROVED THERAPEUTIC USES OF BPI PROTEIN
; PRODUCTS IN CYSTIC FIBROSIS PATIENTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,234
; FILING DATE: 10-Jan-2000
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/962,217
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/742,986
; FILING DATE: 1-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27129/34309
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-480-234-2

Query Match 100.0%; Score 2507; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 1.7e-209;
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAAVNPGVVVRIISQKGLDYASQOQTAALQKEL 60
Db 1 MRENARGPCNAPRWVSLMWLVVAIGTAVTAAVNPGVVVRIISQKGLDYASQOQTAALQKEL 60

Qy 61 KRIKIPDYSDFKIKHLKGHYSFYSMDIRFQLPSSQISWPNVGLKFSISNANIKISG 120
Db 61 KRIKIPDYSDFKIKHLKGHYSFYSMDIRFQLPSSQISWPNVGLKFSISNANIKISG 120

Qy 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180
Db 121 KWKAQKRFKMGSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSHINSVHVHISKS 180

Qy 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPYFQTLPMVTKIDSVAGINYL 240
Db 181 KVGMLIQLFHKKIESALRNKNSQCEKVTNSVSSKLPYFQTLPMVTKIDSVAGINYL 240

Qy 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFFAAHDMVYGLSDYFFNTAGLV 300
Db 241 VAPPATTAETLDVQMKGEFYSENHNPPFPAPPVMEFFAAHDMVYGLSDYFFNTAGLV 300

Qy 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360
Db 301 YQEAGVLKMTLRDDMI PKESKFRLLTKFGTFLPEVAKKFNPMKIQIHVSASTPPHLSVQ 360

Qy 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420
Db 361 PTGLTFYPADVQAFVLPNSSLASLFLIGMHTTGSMEVSAESNRLVGLKLDRLLELK 420

Qy 421 HSNIGPPFVELLDIMNYIVPILVLPVNEKLOKGFPLPTPARVOLYNVVLQPHONFLIF 480
Db 421 HSNIGPPFVELLDIMNYIVPILVLPVNEKLOKGFPLPTPARVOLYNVVLQPHONFLIF 480

```

Qy 481 GADVVYK 487  
| | | | |  
Db 481 GADVVYK 487

Search completed: October 21, 2005, 11:37:01  
Job time : 174.285 secs

STIC-Biotech/ChemLib

169216

me

**From:** Chan, Christina  
**Sent:** Thursday, October 20, 2005 5:15 PM  
**To:** Mitra, Rita; STIC-Biotech/ChemLib  
**Subject:** RE: SEQ search request 10/629516

Please rush. Thanks Chris

Chris Chan  
TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
OCT 21 2005  
STIC/BIOTECH/STIC

-----Original Message-----

**From:** Mitra, Rita  
**Sent:** Thursday, October 20, 2005 4:16 PM  
**To:** Chan, Christina  
**Subject:** SEQ search request 10/629516

I need your approval for this search request.

I would like to request an expedited sequence search for this case because it is due this bi-week. Please search commercial and published patent databases.

10/629516

SEQ ID NO: 2,  
SEQ ID NO: 2, amino acids 10-193

Please print out the result.

Thanks.  
Rita

Rita Mitra, Ph.D.  
Patent Examiner, Art Unit 1653  
U.S. Patent and Trademark Office  
Remsen Bldg, Rm 3B65  
Alexandria, VA 22313  
(571)272-0954  
E-mail: rita.mitra@uspto.gov

3070

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

***This Page Blank (uspto)***